
W P E R L H (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 25 12:25:47 2000; MasPar time 23.67 Seconds
Tabular output not generated. 26.013 Million cell updates/sec

Title: >seqmod
Description: (1-26) from 103.pap
Perfect Score: 140
Sequence: 1 ISTXSLSLDIALXXXLPXMRIVEY 26

Scoring table: PAM 150
Gap 15

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a:geneseq36
l:geneseqp

Statistics: Mean 20.429; Variance 79.314; scale 0.258

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	140	100.0	358	1 W64214	Hyperrecombinogenic va	5.62e-06
2	140	100.0	358	1 W64213	New minshall reca prot	5.62e-06
3	140	100.0	358	1 W64216	Hyperrecombinogenic va	5.62e-06
4	140	100.0	358	1 W64215	Hyperrecombinogenic va	5.62e-06
5	140	100.0	358	1 W64218	Hyperrecombinogenic va	5.62e-06
6	140	100.0	358	1 W64217	Hyperrecombinogenic va	5.62e-06
7	123	87.9	348	1 R40973	reca gene product.	2.63e-04
8	113	80.7	273	1 R79145	Deduced sequence of re	2.43e-03
9	113	80.7	273	1 W44140	Helicobacter pylori re	2.43e-03
10	113	80.7	347	1 W44138	Helicobacter pylori re	2.43e-03
11	99	70.7	344	1 R15141	Reca.	5.22e-02
12	97	69.3	340	1 R33198	Thermus aquaticus RecA	8.03e-02
13	94	67.1	338	1 R90681	B. flavum MJ-233 RecA	1.53e-01
14	90	64.3	438	1 W34668	Arabidopsis thaliana R	3.59e-01
15	72	51.4	389	1 W16842	Rice protein from a ge	1.51e+01
16	65	46.4	453	1 R53467	Tea T-cell transmembra	6.08e+01
17	65	46.4	453	1 R14645	Tea gene product (20.5	6.08e+01
18	65	46.4	453	1 W67475	Human T-cell early act	6.08e+01
19	63	45.0	622	1 R28335	ERR receptor.	8.99e+01
20	63	45.0	622	1 W67474	Murine ecotropic retro	8.99e+01
21	63	45.0	707	1 W22153	ApXB protein.	8.99e+01
22	62	44.3	367	1 R47120	Partial human H13 poly	1.09e+02
23	62	44.3	367	1 W67472	Human retroviral recep	1.09e+02

24	62	44.3	628	1 R54876	Human H13 viral recept	1.09e+02
25	62	44.3	628	1 R54872	Human H13 viral recept	1.09e+02
26	62	44.3	629	1 R25072	H13 gene product.	1.09e+02
27	62	44.3	629	1 R54868	Full-length human H13	1.09e+02
28	62	44.3	629	1 R54870	Human H13 viral recept	1.09e+02
29	62	44.3	629	1 R54871	Human H13 viral recept	1.09e+02
30	62	44.3	629	1 W67473	Human retroviral recep	1.09e+02
31	62	44.3	629	1 R54875	Human H13 viral recept	1.09e+02
32	62	44.3	629	1 R54873	Human H13 viral recept	1.09e+02
33	62	44.3	629	1 R54874	Human H13 viral recept	1.09e+02
34	62	44.3	629	1 R54869	Human H13 viral recept	1.09e+02
35	62	44.3	629	1 R47121	Full-length human H13	1.09e+02
36	62	44.3	1500	1 R30636	hCPSI.	1.09e+02
37	61	43.6	709	1 W33345	Human adenylyl cyclase	1.32e+02
38	61	43.6	1288	1 W61369	Rat 5-oxoprolinase.	1.32e+02
39	61	43.6	2386	1 W13153	S. pombe Rad3 polypept	1.32e+02
40	60	42.9	217	1 W34132	Streptococcus pneumoni	1.61e+02
41	60	42.9	217	1 W83376	Streptococcus pneumoni	1.61e+02
42	59	42.1	41	1 R25796	[Ala13]-Arg23-alpha-he	1.94e+02
43	59	42.1	379	1 W26368	Human kidney inward re	1.94e+02
44	59	42.1	514	1 R95044	Apoptosis participation	1.94e+02
45	59	42.1	1594	1 P81184	Sequence encoded by th	1.94e+02

ALIGNMENTS

RESULT 1
ID W64214 standard; Protein; 358 AA.
AC W64214;
DT 28-APR-1999 (first entry)
DE Hyperrecombinogenic variant reca protein clone 2.
KW Escherichia coli; reca protein; hyperrecombinogenic variant; Minshall;
KW recursive sequence recombination; evolution.
OS Escherichia coli.
PN Synthetic.
PS WO9831837-A1.
PD 23-JUL-1998.
PF 16-JAN-1998; U00852.
PR 17-JAN-1997; US-035054.
PA (MAXY-) MAXYGEN INC.
PI Deicardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,
PI Tobin MB;
DR N-PSDB: V44286.
DR WPI; 98-427565/36.
PT Evolution of whole cells and organisms - by recursive DNA sequence
PT recombination in cells to evolve cells having acquired desired
PT function
PS Example 1; Fig 13; 125pp; English.
CC The present invention provides methods employing iterative cycles of
CC recombination and selection/screening for evolution of whole cells
CC and organisms toward acquisition of desired properties, e.g. for
CC enhanced recombination, genome copy number, and capacity for
CC expression and/or secretion of proteins and secondary metabolites.
CC The present sequence represents a hyperrecombinogenic variant of a
CC reca protein (see w64213), from an example of the present invention.
SQ Sequence 358 AA;

Query Match 100.0% Score 140; DB 1; Length 358;

Best Local Similarity 76.9%; Pred. No. 5.62e-06;

Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

DB 46 ISTXSLSLDIALGAGGILPMGRIVEY 71

QY 1 ISTXSLSLDIALXXXLPXMRIVEY 26

RESULT 2

ID W64213 standard; Protein; 358 AA.

AC W64213;

DT 28-APR-1999 (first entry)

DE New minshall reca protein.

KW Escherichia coli; reca protein; hyperrecombinogenic variant; Minshall;
KW recursive sequence recombination; evolution.

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OS Escherichia coli.
PN WO9831837-Al.
PD 23-JUL-1998.
PF 16-JAN-1998; U00852.
PR 17-JAN-1997; US-035054.
PA (MAXI-) MAXYGEN INC.
PI Delcardayre SB, Minshull J, Ness JE, Patten P, Stemmer WPC,
PI Tobin MB;
DR N-PSDB; V44285.
DR WPI; 98-427565/36.
PT Evolution of whole cells and organisms - by recursive DNA sequence
PT recombination in cells to evolve cells having acquired desired
PT function
PS Example 1; Fig 13; 125pp; English.
CC The present invention provides methods employing iterative cycles of
CC recombination and selection/screening for evolution of whole cells
CC and organisms toward acquisition of desired properties, e.g.
CC enhanced recombination, genome copy number, and capacity for
CC expression and/or secretion of proteins and secondary metabolites.
CC The present sequence represents a wild-type recA protein (designated
CC new Minshall), from an example of the present invention.
SQ Sequence 358 AA;

Query Match 100.0%; Score 140; DB 1; Length 358;
Best Local Similarity 76.9%; Pred. No. 5.62e-06;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 46 ISTGSLSLDIALGAGGLPMGRIVEIY 71
   ||| ||||| ||| |||||
QY 1 ISTXSLSLDIALXXXXLPMXRIEY 26

RESULT 3
ID W64216 standard; Protein; 358 AA.
AC W64216;
DT 28-APR-1999 (first entry)
DE Hyperrecombinogenic variant recA protein clone 5.
KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;
KW recursive sequence recombination; evolution.
OS Escherichia coli.
OS Synthetic.
PN WO9831837-Al.
PD 23-JUL-1998.
PF 16-JAN-1998; U00852.
PR 17-JAN-1997; US-035054.
PA (MAXI-) MAXYGEN INC.
PI Delcardayre SB, Minshull J, Ness JE, Patten P, Stemmer WPC,
PI Tobin MB;
DR N-PSDB; V44288.
DR WPI; 98-427565/36.
PT Evolution of whole cells and organisms - by recursive DNA sequence
PT recombination in cells to evolve cells having acquired desired
PT function
PS Example 1; Fig 13; 125pp; English.
CC The present invention provides methods employing iterative cycles of
CC recombination and selection/screening for evolution of whole cells
CC and organisms toward acquisition of desired properties, e.g.
CC enhanced recombination, genome copy number, and capacity for
CC expression and/or secretion of proteins and secondary metabolites.
CC The present sequence represents a hyperrecombinogenic variant of a
CC recA protein (see w64213), from an example of the present invention.
SQ Sequence 358 AA;

Query Match 100.0%; Score 140; DB 1; Length 358;
Best Local Similarity 76.9%; Pred. No. 5.62e-06;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 46 ISTGSLSLDIALGAGGLPMGRIVEIY 71
   ||| ||||| ||| |||||
QY 1 ISTXSLSLDIALXXXXLPMXRIEY 26

RESULT 4
ID W64215 standard; Protein; 358 AA.
AC W64215;
DT 28-APR-1999 (first entry)
DE Hyperrecombinogenic variant recA protein clone 4.
KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;
KW recursive sequence recombination; evolution.
OS Escherichia coli.
OS Synthetic.
PN WO9831837-Al.
PD 23-JUL-1998.
PF 16-JAN-1998; U00852.
PR 17-JAN-1997; US-035054.
PA (MAXI-) MAXYGEN INC.
PI Delcardayre SB, Minshull J, Ness JE, Patten P, Stemmer WPC,
PI Tobin MB;
DR N-PSDB; V44287.
DR WPI; 98-427565/36.
PT Evolution of whole cells and organisms - by recursive DNA sequence
PT recombination in cells to evolve cells having acquired desired
PT function
PS Example 1; Fig 13; 125pp; English.
CC The present invention provides methods employing iterative cycles of
CC recombination and selection/screening for evolution of whole cells
CC and organisms toward acquisition of desired properties, e.g.
CC enhanced recombination, genome copy number, and capacity for
CC expression and/or secretion of proteins and secondary metabolites.
CC The present sequence represents a hyperrecombinogenic variant of a
CC recA protein (see w64213), from an example of the present invention.
SQ Sequence 358 AA;

Query Match 100.0%; Score 140; DB 1; Length 358;
Best Local Similarity 76.9%; Pred. No. 5.62e-06;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 46 ISTGSLSLDIALGAGGLPMGRIVEIY 71
   ||| ||||| ||| |||||
QY 1 ISTXSLSLDIALXXXXLPMXRIEY 26

RESULT 5
ID W64218 standard; Protein; 358 AA.
AC W64218;
DT 28-APR-1999 (first entry)
DE Hyperrecombinogenic variant recA protein clone 13.
KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;
KW recursive sequence recombination; evolution.
OS Escherichia coli.
OS Synthetic.
PN WO9831837-Al.
PD 23-JUL-1998.
PF 16-JAN-1998; U00852.
PR 17-JAN-1997; US-035054.
PA (MAXI-) MAXYGEN INC.
PI Delcardayre SB, Minshull J, Ness JE, Patten P, Stemmer WPC,
PI Tobin MB;
DR N-PSDB; V44290.
DR WPI; 98-427565/36.
PT Evolution of whole cells and organisms - by recursive DNA sequence
PT recombination in cells to evolve cells having acquired desired
PT function
PS Example 1; Fig 13; 125pp; English.
CC The present invention provides methods employing iterative cycles of
CC recombination and selection/screening for evolution of whole cells
CC and organisms toward acquisition of desired properties, e.g.
CC enhanced recombination, genome copy number, and capacity for
CC expression and/or secretion of proteins and secondary metabolites.
CC The present sequence represents a hyperrecombinogenic variant of a
CC recA protein (see w64213), from an example of the present invention.
SQ Sequence 358 AA;

Query Match 100.0%; Score 140; DB 1; Length 358;
Best Local Similarity 76.9%; Pred. No. 5.62e-06;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 46 ISTGSLSLDIALGAGGLPMGRIVEIY 71
   ||| ||||| ||| |||||
QY 1 ISTXSLSLDIALXXXXLPMXRIEY 26

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Db 46 ISTXSLSLDIALGAGGLPMGRIVEY 71
 ||| ||||| ||| |||||
 QY 1 ISTXSLSLDIALXXXXLPMXRIVEY 26

RESULT 6
 ID W64217 standard; Protein; 358 AA.
 AC W64217;
 DT 28-APR-1999 (first entry)
 DE Hyperrecombinogenic variant recA protein clone 6.
 KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;
 KW recursive sequence recombination; evolution.
 OS Escherichia coli.
 NC Synthetic.
 WO9831837-A1.
 23-JUL-1998.
 PF 16-JAN-1998; U00852.
 PR 17-JAN-1997; US-035054.
 PA (MAXY-) MAXYGEN INC.
 PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,
 PI Tobin MB;
 DR WPI; 98-427565/36.
 DR N-PSDB; V44289.
 DT Evolution of whole cells and organisms - by recursive DNA sequence
 PT recombination in cells to evolve cells having acquired desired
 PT function
 PS Example 1; Fig 13; 125pp; English.
 CC The present invention provides methods employing iterative cycles of
 CC recombination and selection/screening for evolution of whole cells
 CC and organisms toward acquisition of desired properties, e.g.
 CC enhanced recombinogenicity, genome copy number, and capacity for
 CC expression and/or secretion of proteins and secondary metabolites.
 CC The present sequence represents a hyperrecombinogenic variant of a
 CC recA protein (see W64213), from an example of the present invention.
 SQ Sequence 358 AA;

Query Match 100.0%; Score 140; DB 1; Length 358;
 Best Local Similarity 76.9%; Pred. No. 5,62e-06; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 6;

Db 46 ISTXSLSLDIALGAGGLPMGRIVEY 71
 ||| ||||| ||| |||||
 1 ISTXSLSLDIALXXXXLPMXRIVEY 26

RESULT 7
 ID R40973 standard; Protein; 348 AA.
 AC R40973;
 DT 04-MAR-1994 (first entry)
 DE recA gene product.
 KW recA; microbe; acetic acid bacterium.
 OS Acetobacter altoacetigenes.
 PN J0519987-A.
 PD 10-AUG-1993.
 PF 30-JAN-1991; 094678.
 PR 08-FEB-1990; JP-028391.
 PA (NAKA-) NAKANO SUTEN KK.
 DR WPI; 93-284684/36.
 DR N-PSDB; Q48658.
 DT Acetic acid bacterium recA gene - with plasmid contg. it and a
 PT transformed acetic acid bacterium
 PS Claim 1; Page 8-10; 10pp; Japanese.
 CC The recA gene can control the recombination activity of the
 CC acetic acid bacterium gene.
 SQ Sequence 348 AA;

Query Match 87.9%; Score 123; DB 1; Length 348;
 Best Local Similarity 65.4%; Pred. No. 2.63e-04; Indels 0; Gaps 0;
 Matches 17; Conservative 2; Mismatches 7;

Db 43 ISTXSLSLDIALGAGGLPMGRIVEY 68
 ||| ||||| ||| |||||

QY 1 ISTXSLSLDIALXXXXLPMXRIVEY 26

RESULT 8
 ID R79145 standard; Protein; 273 AA.
 AC R79145;
 DT 28-DEC-1995 (first entry)
 DE Deduced sequence of recombinase encoded by H. pylori RecA gene.
 KW Recombinase; recA; Helicobacter pylori.
 OS Helicobacter pylori.
 FH Key Location/Qualifiers
 FT misc_difference 67
 FT /label= conserved in bacterial RecA proteins
 FT misc_difference 73.74
 FT /label= see above
 FT misc_difference 95
 FT /label= see above
 FT misc_difference 97
 FT /label= see above
 FT misc_difference 104
 FT /label= see above
 FT misc_difference 145.146
 FT /label= see above
 FT misc_difference 194.195
 FT /label= see above
 FT misc_difference 213
 FT /label= see above

US5434253-A.
 18-JUL-1995.
 PF 21-MAR-1994; 215928.
 PR 21-MAR-1994; US-215928.
 PA (UYVA-) UNIV VANDERBILT.
 PI Blaser MJ, Thompson SA;
 DR WPI; 95-263283/34.
 DR N-PSDB; Q96252.
 PT Nucleic acid encoding a portion of Helicobacter pylori recombinase
 PT used e.g. for detecting H. pylori or producing recombinant enzyme.
 PS Disclosure; Columns 13-16; 14pp; English.
 CC A genomic library was prepd. in lambdaZAPII from partially
 CC Alu-digested H. pylori 84-183 chromosomal DNA. The PCR-amplified
 CC recA fragment (see Q96253) was used as probe and identified 3
 CC identical clones contg. 2.3 kb inserts. One of these was designated
 CC pSAT101 (Q96251). The deduced AA sequence (R79145) of this ORF
 CC showed high similarity to bacterial RecA proteins when used in
 CC a BLAST search of GenBank. The ORF contd. on pSAT101 does not
 CC contain a termination codon. This ORF, therefore, is approx.
 CC 80% the length of a typical bacterial recA gene. All of the
 CC highly conserved or invariant residues in bacterial RecA proteins
 CC and related bacteriophage and yeast proteins are present and in
 CC the predicted location in the deduced AA sequence of the pSAT101
 CC ORF.
 SQ Sequence 273 AA;

Query Match 80.7%; Score 113; DB 1; Length 273;
 Best Local Similarity 57.7%; Pred. No. 2.43e-03; Indels 0; Gaps 0;
 Matches 15; Conservative 5; Mismatches 6;

Db 41 ISTXSLSLDIALGAGGLPMGRIVEY 66
 ||| ||||| ||| |||||
 QY 1 ISTXSLSLDIALXXXXLPMXRIVEY 26

RESULT 9
 ID W44140 standard; Protein; 273 AA.
 AC W44140;
 DT 05-MAY-1998 (first entry)
 DE Helicobacter pylori recombinase fragment encoded from pSAT101.
 KW Helicobacter pylori; recombinase; enolase; vaccine; mutant; strain;
 KW nonfunctional.
 OS Helicobacter pylori.
 PN US5703219-A.
 PD 30-DEC-1997.
 PF 22-MAY-1995; 446920;

RESULT	11
ID	R15141 standard; Protein; 344 AA.
AC	R15141;
OS	Recombinant repair; amplification.
PN	W09117267-A.
PD	14-NOV-1991.
PF	17-APR-1991; U03626.
PR	07-MAY-1990; US-520321.

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Db      39 IPTGSLGLDALGIGGIIPRGRVTEIF 64
          | : | |||::|| : | : ||:
Qv      1 ISTXSLSDIALXXXXLPMXRIVEIY 26
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CC that directs completed proteins to enter the nucleus. By introducing the
CC into encephalitis, could be removed and replaced by an amino acid sequence



 (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 25 12:30:48 2000; MasPar time 14.95 Seconds
 Tabular output not generated. 191.070 Million cell updates/sec

Title: >seqmod
 Description: (1-26) from 103.pap
 Perfect Score: 140
 Sequence: 1 ISXXSLSLDIALXXXXLPMXRIVEIY 26

Scoring table: PAM 150
 Gap 15

Searched: 702510 seqs, 109899995 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-pending
 1:P9 2:U60 3:U7 4:U80 5:U81 6:U82 7:U83 8:U84A 9:U84B
 10:U85 11:U86 12:U87 13:U88 14:U89 15:U90 16:U91 17:U92
 18:U93 19:U94 20:NEWP 21:NEWU6 22:NEWU6 23:NEWU7
 24:NEWU8 25:NEWU9

Statistics: Mean 23.645; Variance 78.234; scale 0.302

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	140	100.0	26	25	US-09-358-Sequence 1, Applicatio	3.58e-06
2	140	100.0	358	18	US-09-354-Sequence 9, Applicatio	3.58e-06
3	140	100.0	358	18	US-09-354-Sequence 10, Applicati	3.58e-06
4	140	100.0	358	18	US-09-354-Sequence 11, Applicati	3.58e-06
5	140	100.0	358	18	US-09-354-Sequence 8, Applicatio	3.58e-06
6	140	100.0	358	18	US-09-354-Sequence 13, Applicati	3.58e-06
7	140	100.0	358	18	US-09-354-Sequence 15, Applicati	3.58e-06
8	140	100.0	358	18	US-09-354-Sequence 12, Applicati	3.58e-06
9	126	90.0	363	18	US-09-370-Sequence 17, Applicati	1.31e-04
10	124	88.6	355	18	US-09-328-Sequence 7563, Applic	2.18e-04
11	120	85.7	96	2	US-60-096-Sequence 14, Applicati	6.02e-04
12	120	85.7	328	18	US-09-370-Sequence 6, Applicatio	6.02e-04
13	118	84.3	366	2	US-60-128-Sequence 4548, Applic	9.97e-04
14	115	82.1	97	2	US-60-096-Sequence 4, Applicatio	2.12e-03
15	115	82.1	370	18	US-09-370-Sequence 2, Applicatio	2.12e-03
16	115	82.1	425	18	US-09-310-Sequence 8, Applicatio	2.12e-03
17	115	82.1	425	18	US-09-310-Sequence 8, Applicatio	2.12e-03
18	113	80.7	169	14	US-08-393-Sequence 7471, Applic	3.49e-03
19	113	80.7	273	1	PCT-US95-0Sequence 2, Applicatio	3.49e-03
20	113	80.7	343	14	US-08-993-Sequence 7472, Applic	3.49e-03

21	113	80.7	347	13	US-08-992-Sequence 230, Applicat	3.49e-03
22	113	80.7	347	14	US-08-993-Sequence 7473, Applic	3.49e-03
23	113	80.7	409	18	US-09-310-Sequence 4, Applicatio	3.49e-03
24	108	77.1	430	18	US-09-310-Sequence 6, Applicatio	1.21e-02
25	108	77.1	430	18	US-09-310-Sequence 6, Applicatio	1.21e-02
26	102	72.9	380	20	PCT-US99-2Sequence 764, Applicat	5.28e-02
27	99	70.7	147	18	US-09-370-Sequence 4, Applicatio	1.10e-01
28	90	64.3	438	3	US-07-938-Sequence 2, Applicatio	9.49e-01
29	86	61.4	384	18	US-09-310-Sequence 2, Applicatio	2.43e+00
30	86	61.4	384	18	US-09-310-Sequence 2, Applicatio	2.43e+00
31	85	60.7	26	25	US-09-358-Sequence 3, Applicatio	3.07e+00
32	81	57.9	357	19	US-09-450-Sequence 4382, Applic	7.77e+00
33	79	56.4	314	16	US-09-134-Sequence 3591, Applic	1.23e+01
34	72	51.4	360	25	US-09-340-Sequence 7, Applicatio	5.93e+01
35	70	50.0	803	19	US-09-417-Sequence 40324, Applic	9.22e+01
36	69	49.3	575	16	US-09-107-Sequence 3910, Applic	1.15e+02
37	65	46.4	192	25	US-09-497-Sequence 606, Applicat	2.72e+02
38	65	46.4	242	16	US-09-107-Sequence 3774, Applic	2.72e+02
39	65	46.4	347	2	US-60-167-Sequence 16795, Applic	2.72e+02
40	65	46.4	347	2	US-60-164-Sequence 16071, Applic	2.72e+02
41	65	46.4	560	4	US-08-074-Sequence 4, Applicatio	2.72e+02
42	65	46.4	1088	2	US-60-173-Sequence 23774, Applic	2.72e+02
43	65	46.4	1088	2	US-60-173-Sequence 30577, Applic	2.72e+02
44	65	46.4	1157	2	US-60-164-Sequence 18095, Applic	2.72e+02
45	65	46.4	3921	7	US-08-396-Sequence 2, Applicatio	2.72e+02

ALIGNMENTS

RESULT 1
 ID US-09-358-103-1 STANDARD; PRT; 26 AA.

XX xxxxxx

Sequence 1, Application US/09358103B

Sequence 1, Application US/09358103B

GENERAL INFORMATION:

APPLICANT: Roca, Alberto I

TITLE OF INVENTION: Mutants of MAW Motifs of RecA Protein Homologs, Methods of Making Them, and Their Uses

FILE REFERENCE: RecA Homolog Protein & Mutants

CURRENT APPLICATION NUMBER: US/09358103B

CURRENT FILING DATE: 1993-07-21

EARLIER APPLICATION NUMBER: 60/094,071

EARLIER FILING DATE: 1998-07-24

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 26

TYPE: PRT

ORGANISM: Escherichia coli

FEATURE:

NAME/KEY: NON_TER

LOCATION: (1)

FEATURE:

NAME/KEY: NON_TER

LOCATION: (26)..

FEATURE:

NAME/KEY: HELIX

LOCATION: (6)..(12)

OTHER INFORMATION: Alpha-helix B

FEATURE:

NAME/KEY: STRAND

LOCATION: (22)..(26)

OTHER INFORMATION: Beta-strand 1

FEATURE:

NAME/KEY: SIMILAR

LOCATION: (1)..(26)

OTHER INFORMATION: This structure is highly conserved across bacterial RecA and homologous eukaryotic,

CC OTHER INFORMATION: archaeal, and viral proteins; sequence below is
CC OTHER INFORMATION: from E. coli RecA positions 40-65
SQ SEQUENCE 26 AA; 2604 MW; 3614 CN;

Query Match 100.0%; Score 140; DB 25; Length 26;
Best Local Similarity 76.9%; Pred. No. 3.58e-06;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 1 ISTGSLSDIALGAGGLPMGRIVEIY 26
||| |||||||| ||| ||||||||
QY 1 ISTXSLSDIALXXXXXLPKMRIVEIY 26

RESULT 2
ID US-09-354-922-9 STANDARD; PRT; 358 AA.

XX AC xxxxxx

DT DT

DE DE

XX SEQUENCE 9, Application US/09354922

Sequence 9, Application US/09354922

GENERAL INFORMATION:

APPLICANT: DEL CARDAYRE, STEPHEN

APPLICANT: TOBIN, MATTHEW

APPLICANT: NISS, JON E.

APPLICANT: MINSHULL, JEREMY

APPLICANT: PATTEN, PHILLIP

APPLICANT: SUBRAMANIAN, VENKITESWATAN

APPLICANT: CASTLE, LINDA A.

APPLICANT: KREBER, CLAUD M.

APPLICANT: BASS, STEVE

APPLICANT: ZHANG, YING-XIN

APPLICANT: COX, TONY

APPLICANT: HUISMAN, GJALT

APPLICANT: YUAN, LING

APPLICANT: AFFHOLTER, JOSEPH A.

TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE

TITLE OF INVENTION: SEQUENCE RECOMBINATION

FILE REFERENCE: 02-020730US

CURRENT APPLICATION NUMBER: US/09/354,922

CURRENT FILING DATE: 1999-07-15

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 9

LENGTH: 358

TYPE: PRT

ORGANISM: Escherichia coli

SEQUENCE 358 AA; 38464 MW; 626707 CN;

Query Match 100.0%; Score 140; DB 18; Length 358;
Best Local Similarity 76.9%; Pred. No. 3.58e-06;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 46 ISTGSLSDIALGAGGLPMGRIVEIY 71
||| |||||||| ||| ||||||||
QY 1 ISTXSLSDIALXXXXXLPKMRIVEIY 26

RESULT 3
ID US-09-354-922-10 STANDARD; PRT; 358 AA.

XX AC xxxxxx

DT DT

DE DE

XX SEQUENCE 10, Application US/09354922

Sequence 10, Application US/09354922

GENERAL INFORMATION:

APPLICANT: DEL CARDAYRE, STEPHEN

CC APPLICANT: TOBIN, MATTHEW
CC APPLICANT: STEMMER, WILLEM P.C.
CC APPLICANT: NESS, JON E.

CC APPLICANT: MINSHULL, JEREMY
CC APPLICANT: PATTEN, PHILLIP
CC APPLICANT: SUBRAMANIAN, VENKITESWATAN

CC APPLICANT: CASTLE, LINDA A.
CC APPLICANT: KREBER, CLAUD M.
CC APPLICANT: BASS, STEVE

CC APPLICANT: ZHANG, YING-XIN
CC APPLICANT: COX, TONY
CC APPLICANT: HUISMAN, GJALT

CC APPLICANT: YUAN, LING
CC APPLICANT: AFFHOLTER, JOSEPH A.
CC APPLICANT: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE

CC TITLE OF INVENTION: SEQUENCE RECOMBINATION
CC FILE REFERENCE: 02-020730US
CC CURRENT APPLICATION NUMBER: US/09/354,922

CC CURRENT FILING DATE: 1999-07-15
CC NUMBER OF SEQ ID NOS: 15
CC SOFTWARE: PatentIn Ver. 2.0

CC SEQ ID NO 10
CC LENGTH: 358
CC TYPE: PRT

CC ORGANISM: Escherichia coli
CC SEQUENCE 358 AA; 38404 MW; 628187 CN;

Query Match 100.0%; Score 140; DB 18; Length 358;
Best Local Similarity 76.9%; Pred. No. 3.58e-06;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 46 ISTGSLSDIALGAGGLPMGRIVEIY 71
||| |||||||| ||| ||||||||
QY 1 ISTXSLSDIALXXXXXLPKMRIVEIY 26

RESULT 4
ID US-09-354-922-11 STANDARD; PRT; 358 AA.

XX AC xxxxxx

XX DT

XX DE

XX SEQUENCE 11, Application US/09354922

Sequence 11, Application US/09354922

GENERAL INFORMATION:

APPLICANT: DEL CARDAYRE, STEPHEN

APPLICANT: TOBIN, MATTHEW

APPLICANT: NISS, JON E.

APPLICANT: MINSHULL, JEREMY

APPLICANT: PATTEN, PHILLIP

APPLICANT: SUBRAMANIAN, VENKITESWATAN

APPLICANT: CASTLE, LINDA A.

APPLICANT: KREBER, CLAUD M.

APPLICANT: BASS, STEVE

APPLICANT: ZHANG, YING-XIN

APPLICANT: COX, TONY

APPLICANT: HUISMAN, GJALT

APPLICANT: YUAN, LING

APPLICANT: AFFHOLTER, JOSEPH A.

TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE

TITLE OF INVENTION: SEQUENCE RECOMBINATION

FILE REFERENCE: 02-020730US

CURRENT APPLICATION NUMBER: US/09/354,922

CURRENT FILING DATE: 1999-07-15

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 11

LENGTH: 358

TYPE: PRT

ORGANISM: Escherichia coli

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: consensus

CC OTHER INFORMATION: e. coli sequence
SQ SEQUENCE 358 AA; 38490 MW; 627879 CN;

Query Match 100.0%; Score 140; DB 18; Length 358;
Best Local Similarity 76.9%; Pred. No. 3.58e-06;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 46 ISTGSLDIALGAGGLPMGRIVEY 71
||| ||||| ||| |||||
QY 1 ISTXSLDIALXXXXLPMXRIEY 26

RESULT 8
ID US-09-354-922-12 STANDARD; PRT; 358 AA.

XX AC xxxxxx

Sequence 12, Application US/09354922

GENERAL INFORMATION:

APPLICANT: DEL CARDAYRE, STEPHEN

APPLICANT: TOBIN, MATTHEW

APPLICANT: STEMMER, WILLEM P.C.

APPLICANT: NESS, JON E.

APPLICANT: MINSHULL, JEREMY

APPLICANT: PATTEN, PHILLIP

APPLICANT: SUBRAMANIAN, VENKITESWATAN

APPLICANT: CASTLE, LINDA A.

APPLICANT: KREBER, CLAUS M.

APPLICANT: BASS, STEVE

APPLICANT: ZHANG, YING-XIN

APPLICANT: COX, TONY

APPLICANT: HUISMAN, GJALT

APPLICANT: YUAN, LING

APPLICANT: AFFHOLTER, JOSEPH A.

CC TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE

CC FILE REFERENCE: 02-020730US

CC CURRENT APPLICATION NUMBER: US/09/354,922

CC CURRENT FILING DATE: 1999-07-15

CC NUMBER OF SEQ ID NOS: 15

CC SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 12

LENGTH: 358

TYPE: PRT

ORGANISM: Escherichia coli

SQ SEQUENCE 358 AA; 38462 MW; 630763 CN;

Query Match 100.0%; Score 140; DB 18; Length 358;
Best Local Similarity 76.9%; Pred. No. 3.58e-06;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 46 ISTGSLDIALGAGGLPMGRIVEY 71
||| ||||| ||| |||||
QY 1 ISTXSLDIALXXXXLPMXRIEY 26

RESULT 9
ID US-09-370-319-17 STANDARD; PRT; 363 AA.

XX AC xxxxxx

Sequence 17, Application US/09370319

GENERAL INFORMATION:

APPLICANT: Famodu, Layo O.

APPLICANT: Morgante, Michele

CC APPLICANT: Sakai, Hajime
CC TITLE OF INVENTION: DNA Repair Proteins
CC FILE REFERENCE: BB-1204

CC CURRENT APPLICATION NUMBER: US/09/370,319

CC CURRENT FILING DATE: 1999-08-09

CC EARLIER APPLICATION NUMBER: 60/096,239

CC EARLIER FILING DATE: August 12, 1998

CC NUMBER OF SEQ ID NOS: 22

CC SOFTWARE: Microsoft Office 97

SEQ ID NO 17

LENGTH: 363

TYPE: PRT

ORGANISM: Agrobacterium tumefaciens

SQ SEQUENCE 363 AA; 38802 MW; 629047 CN;

Query Match 90.0%; Score 126; DB 18; Length 363;
Best Local Similarity 65.4%; Pred. No. 1.31e-04;
Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 51 VSTGSLDIALGIGGLPKRIEY 76

QY 1 ISTXSLDIALXXXXLPMXRIEY 26

RESULT 10

ID US-09-328-352-7563 STANDARD; PRT; 355 AA.

XX AC xxxxxx

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Query Match	84.3%;	Score 118;	DB 2;	Length 366;
Best Local Similarity	57.7%;	Pred. No. 9.97e-04;		

Query Match 85.7%; Score 2
Best Local Similarity 65.4%; Pred. 2
Matches 17; Conservative 2; M

RESULT 14

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CC APPLICANT: Sakai, Hajime
CC TITLE OF INVENTION: DNA Repair Proteins
CC FILE REFERENCE: BB-1204
CC CURRENT APPLICATION NUMBER: US/09/370,319
CC CURRENT FILING DATE: 1999-08-09
CC EARLIER APPLICATION NUMBER: 60/096,239
CC EARLIER FILING DATE: August 12, 1998
CC NUMBER OF SEQ ID NOS: 22
CC SOFTWARE: Microsoft Office 97
CC SEQ ID NO 2
CC LENGTH: 370
CC TYPE: PRT
CC ORGANISM: Zea mays
CC SEQUENCE 370 AA; 39459 MW; 691195 CN;

Query Match 82.1%; Score 115; DB 18; Length 370;
Best Local Similarity 53.8%; Pred. No. 2,12e-03;
Matches 14; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Db 42 VSTGSLDLDWALGTGLPKGRVVEY 67
   ||| ||| ||| ||| ||| :|||:
On 1 ISTXSLSDIALXXXLPXRRIVEY 26

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Db 41 ISTGSLSDIALGAGGLPMGRIVEY 66
!!! !!!!!!!! !!! !!!!!!!!
QY 1 ISTXSLSDIALXXXXLPMXRIVEY 26

RESULT 2
ENTRY S31481 #type complete
TITLE recombination protein reca - Enterobacter agglomerans
ALTERNATE_NAMES recombinase A
ORGANISM #formal_name Enterobacter agglomerans
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
05-Mar-1999
ACCESSIONS S31481
REFERENCE S31480
#authors Rappold, C.S.J.; Klingmueller, W.
#submission submitted to the EMBL Data Library, January 1993
#description Cloning and sequencing of the reca gene from Enterobacter
#description agglomerans 339.
#accession S31481
#status preliminary
#molecule_type DNA
#residues 1-354 #label RAP
#cross-references GB:L03291; EMBL:219517; NID:gl209306; PID:gl209308
GENETICS
#gene reca
CLASSIFICATION #superfamily recombination protein reca
KEYWORDS ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS
response
FEATURE
67-74 #region nucleotide-binding motif A (P-loop)\
141-146 #region nucleotide-binding motif B\
73 #binding_site ATP (lys) #status predicted
SUMMARY #length 354 #molecular-weight 37898 #checksum 7629

Query Match 100.0%; Score 140; DB 2; Length 354;
Best Local Similarity 76.9%; Pred. No. 3.48e-13;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 41 ISTGSLSDIALGAGGLPMGRIVEY 66
!!! !!!!!!!! !!! !!!!!!!!
QY 1 ISTXSLSDIALXXXXLPMXRIVEY 26

RESULT 3
ENTRY S37586 #type complete
TITLE recombination protein reca - Yersinia pestis
ALTERNATE_NAMES recombinase A
ORGANISM #formal_name Yersinia pestis
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
05-Mar-1999
ACCESSIONS S37586
REFERENCE S37586
#authors Kryukov, V.M.; Suchkov, I.Y.; Sazykin, I.S.; Mishankin, B.N.
#submission submitted to the EMBL Data Library, October 1993
#description Complete nucleotide sequence of Yersinia pestis reca gene.
#accession S37586
#status preliminary
#molecule_type DNA
#residues 1-356 #label KRY
#cross-references EMBL:X75336; NID:g406793; PID:g406794
GENETICS
#gene reca
CLASSIFICATION #superfamily recombination protein reca
KEYWORDS ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS
response
FEATURE
67-74 #region nucleotide-binding motif A (P-loop)\
141-146 #region nucleotide-binding motif B\
73 #binding_site ATP (lys) #status predicted
SUMMARY #length 356 #molecular-weight 37912 #checksum 8556

Query Match 100.0%; Score 140; DB 2; Length 356;
Best Local Similarity 76.9%; Pred. No. 3.48e-13;

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Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 41 ISTGSLDLIALGAGGLPMGRIVEIY 66
   ||| ||||| ||| |||||
QY 1 ISTXSLDLIALXXXXLPMXRIVEIY 26

RESULT 4
ENTRY JQ1461 #type complete
TITLE recombination protein recA - Vibrio anguillarum
ALTERNATE_NAMES recombinationase A
ORGANISM #formal_name Vibrio anguillarum
DATE 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change
05-Mar-1999

ACCESSIONS JQ1461
REFERENCE JQ1461
#authors Tolmasy, M.E.; Gamble, A.E.; Crosa, J.H.
#journal Gene (1992) 110:41-48
#title Characterization of the recA gene of Vibrio anguillarum.
#cross-references MUID:92184113
#accession JQ1461
##molecule_type DNA
##residues 1-348 #label TOL
##cross-references GB:M80525; NID:g155256; PID:g155257
##experimental_source strains 775 and 531A

GENETICS
#gene recA
#description plays an essential role in homologous recombination, in
induction of the SOS response, and in initiation of stable
DNA replication
CLASSIFICATION #superfamily recombination protein recA
KEYWORDS ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS
response

FEATURE
65-72 #region nucleotide-binding motif A (P-loop)\
139-144 #region nucleotide-binding motif B\
256-279 #region ATP binding #status predicted\
71 #binding_site ATP (Lys) #status predicted
SUMMARY #length 348 #molecular-weight 37558 #checksum 5094

Query Match 98.6%; Score 138; DB 2; Length 348;
Best Local Similarity 73.1%; Pred. No. 8.76e-13;
Matches 19; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 39 ISTGSLDLIALGAGGLPMGRIVEIY 64
   ||| ||||| ||| |||||
QY 1 ISTXSLDLIALXXXXLPMXRIVEIY 26

RESULT 5
ENTRY A49929 #type complete
TITLE recombination protein recA - Haemophilus influenzae (strain
Rd KW20)
ALTERNATE_NAMES rec-1 protein; recombinationase A
ORGANISM #formal_name Haemophilus influenzae
DATE 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change
17-Mar-1999

ACCESSIONS A49929; A64080
REFERENCE A49929
#authors Zulty, J.J.; Barcak, G.J.
#journal J. Bacteriol. (1993) 175:7269-7281
#title Structural organization, nucleotide sequence, and regulation
of the Haemophilus influenzae rec-1(+) gene.
#cross-references MUID:94042901
#accession A49929
##molecule_type DNA
##residues 1-354 #label ZUL
##cross-references GB:L07529; NID:g305381; PID:g305382
##experimental_source Rd strain KW20

REFERENCE A64000
#authors Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;

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Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
Fitzhugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton,
M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Sauddek,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann,
J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.;
Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
Science (1995) 269:496-512
Whole-genome random sequencing and assembly of Haemophilus
influenzae Rd.
#cross-references MUID:95350630
#accession A64080
##status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-354 #label TIGR
##cross-references GB:U32741; GB:L42023; NID:g1573582; PID:g1573588;
TIGR:HI0600
##experimental_source Rd strain KW20

GENETICS
#gene recA
#description plays an essential role in homologous recombination, in
induction of the SOS response, and in initiation of stable
DNA replication
CLASSIFICATION #superfamily recombination protein recA
KEYWORDS ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS
response

FEATURE
67-74 #region nucleotide-binding motif A (P-loop)\
141-146 #region nucleotide-binding motif B\
73 #binding_site ATP (Lys) #status predicted
SUMMARY #length 354 #molecular-weight 38132 #checksum 9408

Query Match 92.9%; Score 130; DB 2; Length 354;
Best Local Similarity 65.4%; Pred. No. 3.40e-11;
Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 41 ISTGSLDLIALGAGGLPMGRIVEIY 66
   ||| ||||| ||| |||||
QY 1 ISTXSLDLIALXXXXLPMXRIVEIY 26

RESULT 6
ENTRY I40347 #type complete
TITLE recombination protein recA - Brucella abortus
ALTERNATE_NAMES recombinationase A
ORGANISM #formal_name Brucella abortus
DATE 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
05-Mar-1999

ACCESSIONS I40347
REFERENCE I40347
#authors Tatum, F.M.
#journal Microb. Pathog. (1993) 14:177-185
#title Construction of a Brucella abortus RecA mutant and its
survival in mice.
#cross-references MUID:93309295
#accession I40347
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 1-360 #label RES
##cross-references GB:L00679; NID:g144122; PID:g144123

GENETICS
#gene recA
#description #superfamily recombination protein recA
CLASSIFICATION ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS
KEYWORDS response

FEATURE
77-84 #region nucleotide-binding motif A (P-loop)\
151-156 #region nucleotide-binding motif B\
83 #binding_site ATP (Lys) #status predicted
SUMMARY #length 360 #molecular-weight 38668 #checksum 4930

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response
FEATURE
65-72      #region nucleotide-binding motif A (P-loop)\
139-144    #region nucleotide-binding motif B\
71         #binding_site ATP (Lys) #status predicted
SUMMARY    #length 348 #molecular-weight 36879 #checksum 5795

Query Match          90.7%; Score 127; DB 1; Length 346;
Best Local Similarity 69.2%; Pred. No. 1.32e-10;
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db   39 ISTGSLGLDIALGGPKGRIVEIY 64
QY   1 ISTDLSLDIALXXXXLPXMRIVEIY 26
     ||| ||||| ||| |||||
RESULT      8
ENTRY       recombination protein recA - Legionella pneumophila
TITLE       recombinase A
ALTERNATE_NAMES
ORGANISM    #formal_name Legionella pneumophila
DATE        31-Dec-1993 #sequence_revision 27-Jun-1994 #text_change
              05-Mar-1999
ACCESSIONS  A60989
REFERENCE    Zhao, X.; Dreyfus, L.A.
#authors    FEMS Microbiol. Lett. (1990) 70:227-232
#journal    Expression and nucleotide sequence analysis of the Legionella
            pneumoniae recA gene.
#accession  A60989
#molecule_type DNA
#residues   1-348 #label ZHA
#crosso-references GB:X5453; NID:g48779; PID:g48780
GENETICS    recA
#gene
FUNCTION     plays an essential role in homologous recombination, in
             induction of the SOS response, and in initiation of stable
             DNA replication
CLASSIFICATION superfamily recombination protein recA
KEYWORDS      ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS
             response

FEATURE
65-72      #region nucleotide-binding motif A (P-loop)\
140-145    #region nucleotide-binding motif B\
72         #binding_site ATP (Lys) #status predicted
SUMMARY    #length 348 #molecular-weight 37934 #checksum 1920

Query Match          90.7%; Score 127; DB 1; Length 348;
Best Local Similarity 69.2%; Pred. No. 1.32e-10;
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db   40 ISTGSLGLDIALGGPKGRIVEIY 65
QY   1 ISTDLSLDIALXXXXLPXMRIVEIY 26
     ||| ||||| ||| |||||
RESULT      9
ENTRY       recombination protein recA - Azotobacter vinelandii
TITLE       recombinase A
ALTERNATE_NAMES
ORGANISM    #formal_name Azotobacter vinelandii
DATE        09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change
              05-Mar-1999
ACCESSIONS  JN0321
REFERENCE    Kenkatesh, T.V.; Das, H.K.
#authors    Gene (1992) 113:47-53
#journal    The Azotobacter vinelandii recA gene: sequence analysis and
            regulation of expression.
#cross-references MUID:92225347
#accession  JN0321
#molecule_type DNA
```



```

#title      Characterization of the recA gene from Pseudomonas
#            fluorensens OE 28.3 and construction of a recA mutant.
#cross-references MUID:93195512
#contents   OE 28.3
#accession  A47709
#status     preliminary
#molecule_type nucleic acid
#residues   1-352 ##label DE1
#cross-references GB:M96558; NID:g151529; PID:g151530
#note       sequence extracted from NCBI backbone (NCBIN:127247,
            NCBI:p127248)

CLASSIFICATION
KEYWORDS    #superfamily recombination protein recA
            ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS
            response

FEATURE
55-72       #region nucleotide-binding motif A (P-loop)\
139-144     #region nucleotide-binding motif B\
71          #binding_site ATP (lys) #status predicted
SUMMARY     #length 352 #molecular-weight 37634 #checksum 9671

Query Match          90.7%; Score 127; DB 2; Length 352;
Best Local Similarity 69.2%; Pred. No. 1.32e-10;
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 39 ISTGSLGLDIALGIGLPGKRIVEIY 64
QY 1 ISTXSLSLDIALXXXLPMXRIVEIY 26

RESULT 12
ENTRY   I39509          #type complete
TITLE   recombination protein recA - Acinetobacter calcoaceticus
ALTERNATE_NAMES
ORGANISM #formal_name Acinetobacter calcoaceticus
DATE     19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change
        05-Mar-1999

ACCESSIONS I39509
REFERENCE  I39509
#authors   Gregg-Jolly, L.A.; Ornstons, L.N.
#journal   Mol. Microbiol. (1994) 12:985-992
#title     Properties of Acinetobacter calcoaceticus recA and its
            contribution to intracellular gene conversion.
#cross-references MUID:95020620
#accession I39509
#status    preliminary; translated from GB/EMBL/DDBJ
#molecule_type DNA
#residues  1-349 ##label RES
#cross-references GB:L26100; NID:g440088; PID:g440089

GENETICS
#gene      recA
CLASSIFICATION
KEYWORDS   #superfamily recombination protein recA
            ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS
            response

FEATURE
55-72       #region nucleotide-binding motif A (P-loop)\
139-144     #region nucleotide-binding motif B\
71          #binding_site ATP (lys) #status predicted
SUMMARY     #length 349 #molecular-weight 37815 #checksum 368

Query Match          90.0%; Score 126; DB 2; Length 349;
Best Local Similarity 65.4%; Pred. No. 2.08e-10;
Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 39 VSTGSLTDLIALGIGLPGKRIVEIY 64
QY 1 ISTXSLSLDIALXXXLPMXRIVEIY 26

RESULT 13
ENTRY   S46274          #type complete
TITLE   recombination protein recA - Vibrio cholerae
ALTERNATE_NAMES
ORGANISM #formal_name Vibrio cholerae

```

```

DATE          27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change
17-Mar-1999
ACCESSIONS    S46274
REFERENCE      S46274
#authors      Stroehner, U.H.; Lech, A.J.; Manning, P.A.
#journal      Mol. Gen. Genet. (1994) 244:295-302
#title        Gene sequence of recA(+) and construction of recA mutants of
              Vibrio cholerae.
#cross-references EMBL:X71969; NID:G530269; PID:G530270
#accession     S46274
#status        preliminary
#molecule_type DNA
#residues      1-354 #label STR
#cross-references EMBL:X71969; NID:G530269; PID:G530270
GENETICS
#gene          recA
CLASSIFICATION #superfamily recombination protein recA
KEYWORDS       ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS
              response
FEATURE
65-72          #region nucleotide-binding motif A (P-loop)\
139-144        #region nucleotide-binding motif B\
71             #binding_site ATP (Lys) #status Predicted
#length 354 #molecular-weight 38273 #checksum 1962
SUMMARY
Query Match    90.0%; Score 126; DB 2; Length 354;
Best Local Similarity 72.0%; Pred. No. 2.08e-10;
Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Db 39 ISTGSLDITLGGGLPMGRIVEI 63
   ||| |||||:| ||| |||||
QY 1 ISTXSLDLIALXXXLPMXRIVEI 25

RESULT 14
ENTRY         RQBPM #type complete
TITLE         recombination protein recA - Proteus mirabilis
ALTERNATE_NAMES recombinationase A
ORGANISM      #formal_name Proteus mirabilis
DATE          30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change
05-Mar-1999
ACCESSIONS    S04606
REFERENCE      S04606
#authors      Akaboshi, E.; Yip, M.L.R.; Howard-Flanders, P.
#journal      Nucleic Acids Res. (1989) 17:4390
#title        Nucleotide sequence of the recA gene of Proteus mirabilis.
#cross-references EMBL:89296502
#accession     S04606
#molecule_type DNA
#residues      1-355 #label AKA
#cross-references GB:X14870; NID:G45631; PID:G45632
ETICS
#gene          recA
FUNCTION       plays an essential role in homologous recombination, in
              induction of the SOS response, and in initiation of stable
              DNA replication
CLASSIFICATION #superfamily recombination protein recA
KEYWORDS       ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS
              response
FEATURE
67-74          #region nucleotide-binding motif A (P-loop)\
141-146        #region nucleotide-binding motif B\
73             #binding_site ATP (Lys) #status Predicted
#length 355 #molecular-weight 38219 #checksum 901
SUMMARY
Query Match    90.0%; Score 126; DB 1; Length 355;
Best Local Similarity 69.2%; Pred. No. 2.08e-10;
Matches 18; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
Db 41 ISTGSLDLVALGGLPRGIVEIY 66
   .||| |||||:| ||| |||||
QY 1 ISTXSLDLIALXXXLPMXRIVEIY 26

```

```

RESULT 15
ENTRY         JCL1377 #type complete
TITLE         recombination protein recA - Agrobacterium tumefaciens
ALTERNATE_NAMES recombinationase A
ORGANISM      #formal_name Agrobacterium tumefaciens
DATE          10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change
17-Mar-1999
ACCESSIONS    JCL1377
REFERENCE      JCL1377
#authors      Wardhan, H.; McPherson, M.J.; Harris, C.A.; Sharma, E.;
              Sastry, G.R.K.
#journal      Gene (1992) 121:133-136
#title        Molecular analysis of the recA gene of Agrobacterium
              tumefaciens C58.
#cross-references MUID:93051348
#accession     JCL1377
#molecule_type DNA
#residues      1-363 #label WAR
#cross-references GB:M36776
GENETICS
#gene          recA
FUNCTION       plays an essential role in homologous recombination, in
              induction of the SOS response, and in initiation of stable
              DNA replication
CLASSIFICATION #superfamily recombination protein recA
KEYWORDS       ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS
              response
FEATURE
77-84          #region nucleotide-binding motif A (P-loop)\
151-156        #region nucleotide-binding motif B\
83             #binding_site ATP (Lys) #status Predicted
#length 363 #molecular-weight 38802 #checksum 7164
SUMMARY
Query Match    90.0%; Score 126; DB 2; Length 363;
Best Local Similarity 65.4%; Pred. No. 2.08e-10;
Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Db 51 VSTGSLDLIALGIGLPGRIEYIY 76
   :||| |||||:| ||| |||||
QY 1 ISTXSLDLIALXXXLPMXRIVEIY 26

Search completed: Tue Apr 25 12:26:54 2000
Job time : 8 secs.

```

MPERCH_PP (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.

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MPERCH_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 25 12:27:11 2000; MasPar time 18.89 Seconds

Tabular output not generated. 41,102 Million cell updates/sec

Title: >seq1mod

Description: (1-26) from 103.pcp

Perfect Score: 140

Sequence: 1 ISTXSLSLDIALXXXXLPMXRIIVEY 26

Scoring table: PAM 150

Gap 15

Searched: 82229 seqs, 29864866 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot38

1:swissprot

Statistics: Mean 31.021; Variance 45.862; scale 0.676

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	140	100.0	325	1	RECA_PROVU RECA PROTEIN.	1.05e-15
2	140	100.0	352	1	RECA_ECOLI RECA PROTEIN.	1.05e-15
3	140	100.0	352	1	RECA_SHISO RECA PROTEIN.	1.05e-15
4	140	100.0	354	1	RECA_ENTAG RECA PROTEIN.	1.05e-15
5	140	100.0	354	1	RECA_SERMA RECA PROTEIN.	1.05e-15
6	140	100.0	356	1	RECA_YERPE RECA PROTEIN.	1.05e-15
7	140	100.0	358	1	RECA_XENBV RECA PROTEIN.	1.05e-15
8	138	98.6	348	1	RECA_VIBAN RECA PROTEIN.	3.08e-15
9	135	96.4	354	1	RECA_VIBCH RECA PROTEIN.	1.50e-14
10	131	93.6	354	1	RECA_PASMU RECA PROTEIN.	1.24e-13
11	130	92.9	354	1	RECA_BRAIN RECA PROTEIN.	2.10e-13
12	128	91.4	360	1	RECA_BRUAB RECA PROTEIN.	5.99e-13
13	127	90.7	346	1	RECA_PSEAE RECA PROTEIN.	1.01e-12
14	127	90.7	348	1	RECA_LSPGN RECA PROTEIN.	1.01e-12
15	127	90.7	349	1	RECA_AGOVI RECA PROTEIN.	1.01e-12
16	127	90.7	352	1	RECA_PSEFL RECA PROTEIN.	1.01e-12
17	127	90.7	355	1	RECA_PSEPU RECA PROTEIN.	1.01e-12
18	126	90.0	342	1	RECA_ERWCA RECA PROTEIN.	1.70e-12
19	126	90.0	349	1	RECA_ACICA RECA PROTEIN.	1.70e-12
20	126	90.0	354	1	RECA_PROMI RECA PROTEIN.	1.70e-12
21	126	90.0	363	1	RECA_AGRTU RECA PROTEIN.	1.70e-12
22	125	89.3	361	1	RECA_RHLP RECA PROTEIN.	2.86e-12
23	123	87.9	344	1	RECA_METFL RECA PROTEIN.	8.05e-12

24	123	87.9	348	1	RECA_ACEPO RECA PROTEIN.	8.05e-12
25	123	87.9	351	1	RECA_RHIME RECA PROTEIN.	8.05e-12
26	123	87.9	351	1	RECA_RHILY RECA PROTEIN.	8.05e-12
27	121	86.4	342	1	RECA_METCL RECA PROTEIN.	2.25e-11
28	121	86.4	344	1	RECA_GLUXO RECA PROTEIN.	2.25e-11
29	121	86.4	347	1	RECA_BURCE RECA PROTEIN.	2.25e-11
30	120	85.7	355	1	RECA_RHOCA RECA PROTEIN.	3.77e-11
31	119	85.0	353	1	RECA_AERSA RECA PROTEIN.	6.28e-11
32	118	84.3	343	1	RECA_XANCP RECA PROTEIN.	1.05e-10
33	118	84.3	343	1	RECA_RHOSH RECA PROTEIN.	1.05e-10
34	118	84.3	344	1	RECA_XANCI RECA PROTEIN.	1.05e-10
35	118	84.3	344	1	RECA_XANOR RECA PROTEIN.	1.05e-10
36	118	84.3	348	1	RECA_RHOVI RECA PROTEIN.	1.05e-10
37	115	82.1	274	1	RECA_NEICI RECA PROTEIN (FRAGMENT	4.80e-10
38	115	82.1	274	1	RECA_NEIME RECA PROTEIN (FRAGMENT	4.80e-10
39	115	82.1	340	1	RECA_MYCGE RECA PROTEIN.	4.80e-10
40	115	82.1	348	1	RECA_NEIGO RECA PROTEIN.	4.80e-10
41	115	82.1	711	1	RECA_MYCLE RECA PROTEIN.	4.80e-10
42	113	80.7	340	1	RECA_RICPR RECA PROTEIN.	1.32e-09
43	113	80.7	356	1	RECA_PARDE RECA PROTEIN.	1.32e-09
44	113	80.7	377	1	RECA_SIRVL RECA PROTEIN.	1.32e-09
45	113	80.7	387	1	RECA_LEPBI RECA PROTEIN.	1.32e-09

ALIGNMENTS

RESULT 1
ID RECA_PROVU STANDARD; PRT: 325 AA.
AC P26346;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 15-DEC-1999 (Rel. 39, Last annotation update)

DE RECA PROTEIN.

GN RECA.

OS Proteus vulgaris.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Proteus.

RN [1]

RP SEQUENCE FROM N.A.

RA ZHAO X., MCENTEE K.;

RT "DNA sequence analysis of the recA genes from Proteus vulgaris,

RT Erwinia carotovora, Shigella flexneri and Escherichia coli B/r.";

RL Mol. Gen. Genet. 222:368-376(1990).

CC FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE

CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF

CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT

CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS

CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC

CC CLEAVAGE.

CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.

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 CC or send an email to license@isb-sib.ch).
 CC -----

CC EMBL; X55355; ; NOT_ANNOTATED_CDS.

DR HSP: P03017; 2REB.

DR PROSITE; PS00321; RECA; 1.

DR PFAW; PF00154; RECA; 1.

KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.

FT NP_BIND 67 74 ATP (BY SIMILARITY).

SQ SEQUENCE 325 AA; 34790 MW; D46C9851 CRC32;

Query Match 100.0%; Score 140; DB 1; Length 325;

Best Local Similarity 76.9%; Pred. No. 1.05e-15;

Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

DB 41 ISTXSLSLDIALGAGGLPMXRIIVEY 66

FT HELIX 146 148
 FT HELIX 152 155
 FT HELIX 166 185
 FT TURN 186 186
 FT STRAND 188 193
 FT HELIX 213 218
 FT STRAND 221 233
 FT TURN 234 235
 FT STRAND 236 249
 FT STRAND 257 263
 FT TURN 264 266
 FT STRAND 267 268
 FT HELIX 270 280
 FT TURN 281 282
 FT STRAND 285 287
 FT TURN 288 289
 FT STRAND 290 293
 FT TURN 294 295
 FT STRAND 296 300
 FT HELIX 301 311
 FT HELIX 313 327
 SQ SEQUENCE 352 AA; 37842 MW; A6DE5451 CRC32;

Query Match 100.0%; Score 140; DB 1; Length 352;
 Best Local Similarity 76.9%; Pred. No. 1.05e-15;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 40 ISTGSLSLDIALGAGLPMGRIVEYI 65
 QY 1 ISTXSLSLDIALXXXXLPMXRIEYI 26

RESULT 3
 ID RECA_SHISO STANDARD; PRT; 352 AA.

AC Q9ZF6;
 DT 15-DEC-1999 (Rel. 39, Created)
 DT 15-DEC-1999 (Rel. 39, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE RECA PROTEIN.
 GN RECA.
 OS Shigella sonnei.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Shigella.
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN-KN1H104S;
 RA PARK Y.C., SHIN H.J., KIM Y.C.;
 RT "Cloning and nucleotide sequence of the recA gene from Shigella sonnei KN1H104S."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE.
 CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.

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 CC

DR EMBL; AF10127; AAC72856.1;
 DR PROSITE; PS00321; RECA; 1.
 KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT NP_BIND 66 73 ATP (POTENTIAL).
 SQ SEQUENCE 352 AA; 37799 MW; ADE29D96 CRC32;

Query Match 100.0%; Score 140; DB 1; Length 352;
 Best Local Similarity 76.9%; Pred. No. 1.05e-15;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 40 ISTGSLSLDIALGAGLPMGRIVEYI 65
 QY 1 ISTXSLSLDIALXXXXLPMXRIEYI 26

RESULT 4
 ID RECA_ENTAG STANDARD; PRT; 354 AA.

AC P33037;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE RECA PROTEIN.
 GN RECA.
 OS Enterobacter agglomerans.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Pantoea.
 CC [1]

SEQUENCE FROM N.A.
 RA RAPPOLD C.S.J., KLINGMUELLER W.;

RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE.

CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
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DR EMBL; L03291; AAA91766.1;
 DR PIR; S31481; S31481.
 DR HSSP; P03017; 2REB.
 DR PROSITE; PS00321; RECA; 1.
 DR PFAM; PF00154; reca; 1.
 KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
 FT NP_BIND 67 74 ATP (BY SIMILARITY).
 SQ SEQUENCE 354 AA; 37898 MW; 629E3B60 CRC32;

Query Match 100.0%; Score 140; DB 1; Length 354;
 Best Local Similarity 76.9%; Pred. No. 1.05e-15;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 41 ISTGSLSLDIALGAGLPMGRIVEYI 66
 QY 1 ISTXSLSLDIALXXXXLPMXRIEYI 26

RESULT 5
 ID RECA_SERMA STANDARD; PRT; 354 AA.

AC P17479;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE RECA PROTEIN.
 GN RECA.

OS Serratia marcescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Serratia.
 CC [1]
 CC SEQUENCE FROM N.A.
 RC STRAIN-SM6;
 RX MEDLINE; 90094239.

RA BALL T.K., WASMUTH C.R., BRAUNAGEL S.C., BENEDIK M.J.;
 RT "Expression of Serratia marcescens extracellular proteins requires
 reca".
 RL J. Bacteriol. 172:342-349(1990).
 CC -1- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
 CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
 CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
 CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
 CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
 CC CLEAVAGE.
 CC -1- SIMILARITY: BELONGS TO THE RECA FAMILY.
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 CC EMBL: M22935; AAA26567.1; --
 DR HSSP: P03017; 2REB.
 DR PROSITE: PS00321; RECA; 1.
 KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
 FT NP_BIND 67 74 ATP (BY SIMILARITY)
 SQ SEQUENCE 354 AA; 37909 MW; 2BC62FDE CRC32;
 Query Match 100.0%; Score 140; DB 1; Length 354;
 Best Local Similarity 76.9%; Pred. No. 1.05e-15;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Db 41 ISTGSLSLDIALGAGGLPMGRIVEY 66
 QY 1 ISTXSLSLDIALXXXLPMXRIVEY 26
 RESULT 6
 ID RECA.YERPE STANDARD; PRT; 356 AA.
 AC P37858;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE RECA PROTEIN.
 GN RECA.
 OS Versinia pestis.
 OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Versinia.
 RN [1]
 RP SEQUENCE FROM N.A.
 STRAIN=231;
 Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
 CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
 CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
 CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
 CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
 CC CLEAVAGE.
 CC -1- SIMILARITY: BELONGS TO THE RECA FAMILY.
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 CC EMBL: X75336; CAA53084.1; --
 DR HSSP: P03017; 2REB.
 DR PROSITE: PS00321; RECA; 1.

DR PFAM: PF00154; reca; 1.
 KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
 FT NP_BIND 67 74 ATP (BY SIMILARITY).
 SQ SEQUENCE 356 AA; 37912 MW; 60B356BF CRC32;
 Query Match 100.0%; Score 140; DB 1; Length 356;
 Best Local Similarity 76.9%; Pred. No. 1.05e-15;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Db 41 ISTGSLSLDIALGAGGLPMGRIVEY 66
 QY 1 ISTXSLSLDIALXXXLPMXRIVEY 26
 RESULT 7
 ID RECA.XENBV STANDARD; PRT; 358 AA.
 AC P96185;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-DEC-1999 (Rel. 39, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE RECA PROTEIN.
 GN RECA.
 OS Xenorhabdus bovienii.
 OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Xenorhabdus.
 RN [1]
 RP SEQUENCE FROM N.A.
 STRAIN=T28/1.
 RA PINYON R.A., GRMSBY R., RALSTON H., THOMAS C.J.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
 CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
 CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
 CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
 CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
 CC CLEAVAGE.
 CC -1- SIMILARITY: BELONGS TO THE RECA FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL: U87924; AAD12585.1; --
 DR HSSP: P03017; 2REB.
 DR PROSITE: PS00321; RECA; 1.
 KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
 FT NP_BIND 67 74 ATP (POTENTIAL).
 SQ SEQUENCE 358 AA; 38487 MW; 3587853C CRC32;
 Query Match 100.0%; Score 140; DB 1; Length 358;
 Best Local Similarity 76.9%; Pred. No. 1.05e-15;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Db 41 ISTGSLSLDIALGAGGLPMGRIVEY 66
 QY 1 ISTXSLSLDIALXXXLPMXRIVEY 26
 RESULT 8
 ID RECA.VIBAN STANDARD; PRT; 348 AA.
 AC P26348;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE RECA PROTEIN.
 GN RECA.
 OS Vibrio anguillarum.
 OS Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrrio.

```

RN  SEQUENCE FROM N.A.
RX  MEDLINE; 92236419.
RA  GAMMIE A.E., CROSA J.H.;
RT  "Co-operative autoregulation of a replication protein gene.";
RL  Mol. Microbiol. 5:3015-3023(1991).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN-775 AND 531A;
RX  MEDLINE; 92184113.
RA  TOLMASKY M.E., GAMMIE A.E., CROSA J.H.;
RT  "Characterization of the recA gene of Vibrio anguillarum.";
RL  Gene 110:41-48(1992).
CC  -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
      PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
      SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
      HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
      WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
      CLEAVAGE.
CC  -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
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CC  EMBL; M80525; AAA27554.1; -
DR  PIR; JQ1461; JQ1461.
DR  HSSP; P03017; 2REB.
DR  PROSITE; PS00321; RECA; 1.
DR  PFAM; PF00154; RECA; 1.
KW  DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
FT  NP_BIND 65 72 ATP (BY SIMILARITY).
SQ  SEQUENCE 348 AA; 37558 MW; FD418A1D CRC32;

Query Match 98.6%; Score 138; DB 1; Length 348;
Best Local Similarity 73.1%; Pred. No. 3,05e-15;
Matches 19; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 39 ISTGSLSLDIALGAGLPMGRIVEY 64
    ||| ||||| ||| |||||
    1 ISTXSLSLDIALXXXXLPMXRIVEY 26

RESULT 9
ID RECA_VIBCH STANDARD; PRT; 354 AA.
AC P45383;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-2740-80;
RX MEDLINE; 95129908.
RA MARGRAF R.L., ROCA A.I., COX M.M.;
RT "The deduced Vibrio cholerae RecA amino-acid sequence.";
RL Gene 152:135-136(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-O17;
RX MEDLINE; 94335880.
RA STROEHER U.H., LECH A.J., MANNING P.A.;
RT "Gene sequence of recA+ and construction of recA mutants of Vibrio
RT cholerae.";
RL Mol. Gen. Genet. 244:295-301(1994).
RN [3]

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RP REVISIONS TO 27: 49; 52 AND 64.
RX MEDLINE; 95129908.
RA MANNING P.A.;
RL Unpublished results, cited by:
RL MARGRAF R.L., ROCA A.I., COX M.M.;
RL Gene 152:135-136(1995).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-569B;
RA BHASIN N., GUPTA N., GHOSH A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
      PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
      SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
      HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
      WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
      CLEAVAGE.
CC  -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
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CC  EMBL; U10162; AAC43291.1; -
DR  EMBL; X71969; CAA50764.1; ALT_SEQ.
DR  EMBL; L42384; AAB59100.1; -
DR  HSSP; P03017; 2REB.
DR  PROSITE; PS00321; RECA; 1.
DR  PFAM; PF00154; RECA; 1.
KW  DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
FT  NP_BIND 65 72 ATP (POTENTIAL).
FT  CONFLICT 94 94 A -> T (IN REF. 2).
SQ  SEQUENCE 354 AA; 38250 MW; DF2E49E9 CRC32;

Query Match 96.4%; Score 135; DB 1; Length 354;
Best Local Similarity 73.1%; Pred. No. 1.50e-14;
Matches 19; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 39 ISTGSLSLDIALGAGLPMGRIVEIF 64
    ||| ||||| ||| |||||
    1 ISTXSLSLDIALXXXXLPMXRIVEY 26

QY 1 ISTXSLSLDIALXXXXLPMXRIVEY 26

RESULT 10
ID RECA_PASMU STANDARD; PRT; 354 AA.
AC P95526;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-2,5;
RX BARBE GARCIA J.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
      PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
      SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
      HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
      WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
      CLEAVAGE.
CC  -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
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DR EMBL: X99324; CAA67699.1; -
 DR HSP: P03017; 2REB.
 DR PROSITE: PS00321; RECA; 1.
 DR PFAM: PF00154; RECA; 1.
 KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
 FT NP_BIND 67 74 ATP (POTENTIAL).
 SQ SEQUENCE 354 AA; 37906 MW; 27DEED66 CRC32;

Query Match 93.6%; Score 131; DB 1; Length 354;
 Best Local Similarity 65.4%; Pred. No. 1.24e-13;
 Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 41 VSTGSLSLDVALGIGLPMGRIVEIF 66
 QY 1 ISTXSLSLDIALXXXXLPMXRIEY 26

RESULT 11

ID RECA_HAEIN STANDARD; PRT; 354 AA.
 AC P43705;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE RECA PROTEIN (RECOMBINASE).
 GN RECA OR RECI OR HI0600.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RD;
 RX MEDLINE: 95350630.
 RA ZULY J.J., BARCA G.J.;
 RT "Structural organization, nucleotide sequence, and regulation of the
 RT Haemophilus influenzae rec-1+ gene."
 RL J. Bacteriol. 175:7269-7281(1993).

[2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RD / KW20;
 RX MEDLINE: 95350630.
 RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
 RA KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
 RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
 RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODE A., KELLEY J.M.,
 RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLUM E., COTTON M.D.,
 RA UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
 RA FINE L.D., FRITZMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
 RA GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
 RA VENTER J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 RT influenzae Rd."
 RL Science 269:496-512(1995).

CC -1- FUNCTION: PLAYS A CENTRAL ROLE IN DNA METABOLISM, PARTICIPATING IN
 CC GENERAL HOMOLOGOUS RECOMBINATION, RECOMBINATIONAL
 CC (POSTREPLICATION) DNA REPAIR, AND PHAGE INDUCTION.
 CC -1- SIMILARITY: BELONGS TO THE RECA FAMILY.

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DR EMBL: L07529; AAC36817.1; -
 DR EMBL: U32741; AAC22257.1; -

DR HSP: P03017; 2REB.
 DR TIGR: HI0600; -
 DR PROSITE: PS00321; RECA; 1.
 DR PFAM: PF00154; RECA; 1.
 KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
 FT NP_BIND 67 74 ATP (POTENTIAL).
 SQ SEQUENCE 354 AA; 38132 MW; 52D4E68E CRC32;

Query Match 92.9%; Score 130; DB 1; Length 354;
 Best Local Similarity 65.4%; Pred. No. 2.10e-13;
 Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 41 ISTGSLSLDVALGIGLPMGRIVEIF 66
 QY 1 ISTXSLSLDIALXXXXLPMXRIEY 26

RESULT 12

ID RECA_BRUAB STANDARD; PRT; 360 AA.
 AC Q04761;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE RECA PROTEIN.
 GN RECA.
 OS Brucella abortus.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Brucella.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93309295.
 RA TATUM F.M.;
 RT "Construction of a Brucella abortus RecA mutant and its survival in
 RT mice."
 RL Microb. Pathog. 14:177-185(1993).
 CC -1- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
 CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
 CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
 CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
 CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
 CC CLEAVAGE.
 CC -1- SIMILARITY: BELONGS TO THE RECA FAMILY.

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DR EMBL: L00679; AAA22999.1; -
 DR HSP: P03017; 2REB.
 DR PROSITE: PS00321; RECA; 1.
 DR PFAM: PF00154; RECA; 1.
 KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
 FT NP_BIND 77 84 ATP (BY SIMILARITY).
 SQ SEQUENCE 360 AA; 38668 MW; 6DBDF223 CRC32;

Query Match 91.4%; Score 128; DB 1; Length 360;
 Best Local Similarity 69.2%; Pred. No. 5.99e-13;
 Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 51 VSTGSLSLDIALGVLGPKRIVEIF 76
 QY 1 ISTXSLSLDIALXXXXLPMXRIEY 26

RESULT 13

ID RECA_PSEAE STANDARD; PRT; 346 AA.
 AC P08280;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)


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DE 15-DEC-1999 (Rel. 39, Last annotation update)
DN RECA.
GN Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
OC Pseudomonas.
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-PAO;
RX MEDLINE; 88038334.
RA SANO Y., KAGEYAMA M.;
RT "The sequence and function of the recA gene and its protein in
RT Pseudomonas aeruginosa PAO.";
RT Mol. Gen. Genet. 208:412-419(1987).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN-PAM 7;
RL ZAITSEV E.N., KRJUKOV V.M., KUZMIN N.P., ALEKSEEV A.A., LANZOV V.A.;
RL Submitted (MAR-1990) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RX MEDLINE; 91182156.
RA KRIJUKOV V.M., ZAITSEV E.N., KOUZMIN N.P., BAYEV A.A.;
RA "Structure of the Pseudomonas aeruginosa recA gene.";
RA Bioorg. Khim. 16:1177-1182(1990).
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
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CC -----
DR EMBL; X05691; CAA39173.1; -
DR EMBL; X52261; CAA36504.1; -
DR PIR; S06265; ROPSAA.
DR PIR; S10458; S10458.
DR PIR; JN0304; JN0304.
DR HSP; P03017; 2REB.
DR PROSITE; PS00321; RECA; 1.
DR PFAM; PF00154; recA; 1.
DR NP_BIND 65 72
FT CONFLICT 333 333 V -> L (IN REF. 3).
SQ SEQUENCE 346 AA; 36879 MW; 314B7320 CRC32;

Query Match 90.7%; Score 127; DB 1; Length 346;
Best Local Similarity 69.2%; Pred. No. 1.01e-12;
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 39 ISTGSLGLDIALGIGGPKGRIVEY 64
QY 1 ISTXSLSLDIALXXXLPMAIVEY 26

RESULT 14
ID RECA.LEGPN STANDARD; PRT; 348 AA.
AC Q05358;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae;

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OC Legionella.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91032890.
RA ZHAO X., DREYFUS L.A.;
RT "Expression and nucleotide sequence analysis of the Legionella
RT FEMS Microbiol. Lett. 58:227-231(1990).
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
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CC -----
DR EMBL; X55453; CAA39097.1; -
DR EMBL; X55453; CAA39098.1; ALT_INIT.
DR PIR; A60889; A60889.
DR HSP; P03017; 2REB.
DR PROSITE; PS00321; RECA; 1.
DR PFAM; PF00154; recA; 1.
DR NP_BIND 66 73
FT CONFLICT 333 333 V -> L (IN REF. 3).
SQ SEQUENCE 348 AA; 37934 MW; 3BE3214 CRC32;

Query Match 90.7%; Score 127; DB 1; Length 348;
Best Local Similarity 69.2%; Pred. No. 1.01e-12;
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 40 ISTGSLGLDIALGIGGPKGRIVEY 65
QY 1 ISTXSLSLDIALXXXLPMAIVEY 26

RESULT 15
ID RECA.AZOVI STANDARD; PRT; 349 AA.
AC P29246;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; gamma subdivision; Azotobacteraceae;
OC Azotobacter.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92225347.
RA VENKATESH T.V., DAS H.K.;
RT "The Azotobacter vinelandii recA gene: sequence analysis and
RT regulation of expression.";
RL Gene 113:47-53(1992).
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
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DR EMBL; S96898; CAB34553.1; -.
DR PIR; JN0321; JN0321.
DR HSSP; P03017; 2REB.
DR PROSITE; PS00321; RECA; 1.
DR PFAM; PF00154; RECA; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
FT NP_BIND 65 72 ATP (BY SIMILARITY).
SQ SEQUENCE 349 AA; 37203 MW; B4EB0D97 CRC32;

Query Match 90.7%; Score 127; DB 1; Length 349;
Best Local Similarity 69.2%; Pred. No. 1.01e-12;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 39 ISTGSLGLDIALGIGLPKGRIVEIY 64
||| ||||| ||: |||||
QY 1 ISTXSLSLDIALXXXXLPMXRIVEIY 26

rch completed: Tue Apr 25 12:27:55 2000
time : 44 secs.

! FINDPATTERNS on geneseq: * allowing 0 mismatches

! 1 IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)

W64215 ck: 6091 len: 358 ! Hyperrecombinogenic variant recA protein cl
IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)
46: MDVET IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
ISTGSLSDIALGAGGLPMGRIVEIY GPSS

W64216 ck: 5676 len: 358 ! Hyperrecombinogenic variant recA protein cl
IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)
46: MDVET IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
ISTGSLSDIALGAGGLPMGRIVEIY GPSS

W64217 ck: 6188 len: 358 ! Hyperrecombinogenic variant recA protein cl
IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)
46: MDVET IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
ISTGSLSDIALGAGGLPMGRIVEIY GPSS

W64218 ck: 6188 len: 358 ! Hyperrecombinogenic variant recA protein cl
IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)
46: MDVET IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
ISTGSLSDIALGAGGLPMGRIVEIY GPSS

W64213 ck: 6469 len: 358 ! New minshall recA protein. Evolution of who
IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)
46: MDVET IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
ISTGSLSDIALGAGGLPMGRIVEIY GPSS

W64214 ck: 7100 len: 358 ! Hyperrecombinogenic variant recA protein cl
IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)
46: MDVET IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
ISTGSLSDIALGAGGLPMGRIVEIY GPSS

Databases searched:

GeneSeq, Release 36.3, Released on 8Jul1999, Formatted on 9Jul1999

Total finds: 6
Total length: 23,686,106
Total sequences: 188,963
CPU time: 02:20.08

!!AA_SEQUENCE 1.0

ID W64215 standard; Protein; 358 AA.

AC W64215;

DT 28-APR-1999 (first entry)

DE Hyperrecombinogenic variant recA protein clone 4.

KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;

KW recursive sequence recombination; evolution.

OS Escherichia coli.

PN WO9831837-A1.

PF 23-JUL-1998.

PR 16-JAN-1998; U00852.

PA (MAXY-) MAXYGEN INC.

PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,

DR WPI; 98-427565/36.

DR N-PSDB; V44287.

PT Evolution of whole cells and organisms - by recursive DNA sequence
PT recombination in cells to evolve cells having acquired desired
PT function

PS Example 1; Fig 13; 125pp; English.

CC The present invention provides methods employing iterative cycles of
CC recombination and selection/screening for evolution of whole cells
CC and organisms toward acquisition of desired properties, e.g.
CC enhanced recombinogenicity, genome copy number, and capacity for
CC expression and/or secretion of proteins and secondary metabolites.
CC The present sequence represents a hyperrecombinogenic variant of a
CC recA protein (see w64213), from an example of the present invention.
SQ Sequence 358 AA;

W64215 Length: 358 April 26, 2000 08:15 Type: P Check: 6091

1 MTGVNMAIDE NKOKALAAAL GOIEKQFGKG SIMRLGEDRC MDVETISTGS

51 LSLDIALGAG GLPMGRIVEI YGPSSGKTT LTLOVIAAAQ REGKTCAFID

101 AEHALDPIYA RLGVVDIDNL LCSQPDGEGQ ALEICDALAR SGAVDVIVVE

151 SVAALTPKAE IEGEIGDSHM GLAARMMSQA MRKLGNLQKQ SNTLLIFINQ

201 IRMKIGVMFG NPETTTGGNA LKFYASVRLD IRRIGAVKEG ENVVGSSETR

251 KVVKNKTAAP FKQAEFQILY GEGINFYGEL VDLGVKEKLI EKAGAWYSYK

301 GEKVGOCKAN ATAWLKDNP TAKEIEKKVR ELLLSNPNST PDFSVDDSEG

351 VAETNEDEF

!!AA_SEQUENCE 1.0

ID W64216 standard; Protein; 358 AA.

AC W64216;

DT 28-APR-1999 (first entry)

DE Hyperrecombinogenic variant recA protein clone 5.

KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;

KW recursive sequence recombination; evolution.

OS Escherichia coli.

OS Synthetic.

PN WO9831837-A1.

PD 23-JUL-1998.

PF 16-JAN-1998; U00852.

PR 17-JAN-1997; US-035054.

PA (MAXY-) MAXYGEN INC.

PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,

DR WPI; 98-427565/36.

DR N-PSDB; V44288.

PT Evolution of whole cells and organisms - by recursive DNA sequence

PT recombination in cells to evolve cells having acquired desired

PT function

PS Example 1; Fig 13; 125pp; English.

CC The present invention provides methods employing iterative cycles of
CC recombination and selection/screening for evolution of whole cells
CC and organisms toward acquisition of desired properties, e.g.
CC enhanced recombinogenicity, genome copy number, and capacity for
CC expression and/or secretion of proteins and secondary metabolites.
CC The present sequence represents a hyperrecombinogenic variant of a
CC recA protein (see w64213), from an example of the present invention.
SQ Sequence 358 AA;

W64216 Length: 358 April 26, 2000 08:15 Type: P Check: 5676

1 MTGVNMAIDE NKOKALAAAL GOIEKQFGKG SIMRLGEDRS MDVETISTGS

51 LSLDIALGAG GLPMGRIVEI YGPSSGKTT LTLOVIAAAQ REGKTCAFID

101 AEHALDPIYA RLGVVDIDNL LCSQPDGEGQ ALEICDALAR SGAVDVIVVE

151 SVAALTPKAE IEGEIGDSHM GLAARMMSQA MRKLGNLQKQ SNTLLIFINQ

201 IRMKIGVMFG NPETTTGGNA LKFYASVRLD IRRIGAVKEG ENVVGSSETR

251 KVVKNKIAAP FKQAEFQILY DEGINFYGEL VDLGVKELI EKAGAWYSYK
 301 GEKAGOGKAN AAWLKGNP TAKEIEKKVR ELLLSNPST PDFSVDDSEG
 351 VAETNEDE

!!AA_SEQUENCE 1.0
 ID W64217 standard; Protein: 358 AA.
 AC W64217;
 DT 28-APR-1999 (first entry)
 DE Hyperrecombinogenic variant reca protein clone 6.
 KW Escherichia coli; reca protein; hyperrecombinogenic variant; Minshall;
 KW recursive sequence recombination; evolution.
 OS Escherichia coli.
 OS Synthetic.
 PN WO9831837-Al.
 PD 23-JUL-1998.
 PF 16-JAN-1998; U00852.
 PR 17-JAN-1997; US-035054.
 PA (MAXY-) MAXYGEN INC.
 PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,
 Tobin MB;
 WPI: 98-427565/36.
 N-PSDB; V44280.
 PT Evolution of whole cells and organisms - by recursive DNA sequence
 PT recombination in cells to evolve cells having acquired desired
 PT function
 PS Example 1; Fig 13; 125pp; English.
 CC The present invention provides methods employing iterative cycles of
 CC recombination and selection/screening for evolution of whole cells
 CC and organisms toward acquisition of desired properties, e.g.
 CC enhanced recombinogenicity, genome copy number, and capacity for
 CC expression and/or secretion of proteins and secondary metabolites.
 CC The present sequence represents a hyperrecombinogenic variant of a
 CC reca protein (see W64213), from an example of the present invention.
 CC Sequence 358 AA;
 SQ

W64217 Length: 358 April 26, 2000 08:15 Type: P Check: 6188 ..
 1 MTGVKMAIDE NKQKALAAAL GQIEKQFGKG SIMRLGEDRS MDVETISTGS
 51 LSLDIALGAG GLPMGRIVEI YGPESGKTT LTLOVIAAAQ REGKTCAFID
 101 AEHALDPIYA RKLGVDDIDNL LCSQPTDGEQ ALEICDALAR SGAVDVIWVE
 151 SVAALTPKAE IEGEIGDSHM GLAARMMSQA MRKLGNLQK SNTLLIFINQ
 201 IRMKIGVMFG NPETTTGGNA LKFYASVRLD IRRIGAVKEG ENVVGSETRV
 251 KVVKNKIAAP FKQAEFQILY DEGINFYGEL VDLGVKELI EKAGAWYSYK
 301 GEKAGOGKAN ATAWLKDNP TAKEIEKKVR ELLLSNPST PDFSVDDSEG
 351 VAETNEDE

!!AA_SEQUENCE 1.0
 ID W64218 standard; Protein: 358 AA.
 AC W64218;
 DT 28-APR-1999 (first entry)
 DE Hyperrecombinogenic variant reca protein clone 13.
 KW Escherichia coli; reca protein; hyperrecombinogenic variant; Minshall;
 KW recursive sequence recombination; evolution.
 OS Escherichia coli.
 OS Synthetic.
 PN WO9831837-Al.
 PD 23-JUL-1998.
 PF 16-JAN-1998; U00852.
 PR 17-JAN-1997; US-035054.
 PA (MAXY-) MAXYGEN INC.
 PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,
 Tobin MB;
 WPI: 98-427565/36.
 DR

DR N-PSDB; V44290.
 PT Evolution of whole cells and organisms - by recursive DNA sequence
 PT recombination in cells to evolve cells having acquired desired
 PT function
 PS Example 1; Fig 13; 125pp; English.
 CC The present invention provides methods employing iterative cycles of
 CC recombination and selection/screening for evolution of whole cells
 CC and organisms toward acquisition of desired properties, e.g.
 CC enhanced recombinogenicity, genome copy number, and capacity for
 CC expression and/or secretion of proteins and secondary metabolites.
 CC The present sequence represents a hyperrecombinogenic variant of a
 CC reca protein (see W64213), from an example of the present invention.
 CC Sequence 358 AA;
 SQ

W64218 Length: 358 April 26, 2000 08:15 Type: P Check: 6188 ..
 1 MTGVKMAIDE NKQKALAAAL GQIEKQFGKG SIMRLGEDRS MDVETISTGS
 51 LSLDIALGAG GLPMGRIVEI YGPESGKTT LTLOVIAAAQ REGKTCAFID
 101 AEHALDPIYA RKLGVDDIDNL LCSQPTDGEQ ALEICDALAR SGAVDVIWVE
 151 SVAALTPKAE IEGEIGDSHM GLAARMMSQA MRKLGNLQK SNTLLIFINQ
 201 IRMKIGVMFG NPETTTGGNA LKFYASVRLD IRRIGAVKEG ENVVGSETRV
 251 KVVKNKIAAP FKQAEFQILY DEGINFYGEL VDLGVKELI EKAGAWYSYK
 301 GEKAGOGKAN ATAWLKDNP TAKEIEKKVR ELLLSNPST PDFSVDDSEG
 351 VAETNEDE

!!AA_SEQUENCE 1.0
 ID W64213 standard; Protein: 358 AA.
 AC W64213;
 DT 28-APR-1999 (first entry)
 DE New Minshall reca protein.
 KW Escherichia coli; reca protein; hyperrecombinogenic variant; Minshall;
 KW recursive sequence recombination; evolution.
 OS Escherichia coli.
 PN WO9831837-Al.
 PD 23-JUL-1998.
 PF 16-JAN-1998; U00852.
 PR 17-JAN-1997; US-035054.
 PA (MAXY-) MAXYGEN INC.
 PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,
 Tobin MB;
 WPI: 98-427565/36.
 DR N-PSDB; V44285.
 PT Evolution of whole cells and organisms - by recursive DNA sequence
 PT recombination in cells to evolve cells having acquired desired
 PT function
 PS Example 1; Fig 13; 125pp; English.
 CC The present invention provides methods employing iterative cycles of
 CC recombination and selection/screening for evolution of whole cells
 CC and organisms toward acquisition of desired properties, e.g.
 CC enhanced recombinogenicity, genome copy number, and capacity for
 CC expression and/or secretion of proteins and secondary metabolites.
 CC The present sequence represents a wild-type reca protein (designated
 CC new Minshall), from an example of the present invention.
 CC Sequence 358 AA;
 SQ

W64213 Length: 358 April 26, 2000 08:15 Type: P Check: 6469 ..
 1 MTGVKMAIDE NKQKALAAAL GQIEKQFGKG SIMRLGEDRS MDVETISTGS
 51 LSLDIALGAG GLPMGRIVEI YGPESGKTT LTLOVIAAAQ REGKTCAFID
 101 AEHALDPIYA RKLGVDDIDNL LCSQPTDGEQ ALEICDALAR SGAVDVIWVE
 151 SVAALTPKAE IEGEIGDSHM GLAARMMSQA MRKLGNLQK SNTLLIFINQ
 201 IRMKIGVMFG NPETTTGGNA LKFYASVRLD IRRIGAVKEG ENVVGSETRV

251 KVVKNKIAAP FKQAEFQILY GEGINFYGEL VDLGVKEKLI EKAGAWYSYK
 301 GEKIGOGKAN ATAWLKDNPE TAKEIEKKVR ELLLSNPNST PDFSVDDSEG
 351 VAETNEDE

!!AA_SEQUENCE 1.0

ID W64214 standard; Protein: 358 AA.

AC W64214;

DT 28-APR-1999 (first entry)

DE Hyperrecombinogenic variant reca protein clone 2.

KW Escherichia coli; reca protein; hyperrecombinogenic variant; Minshall;

KW recursive sequence recombination; evolution.

Escherichia coli.

Synthetic.

WO9831837-A1.

23-JUL-1998.

PF 16-JAN-1998; U00852.

PR 17-JAN-1997; US-035054.

PA (MAXY-) MAXYGEN INC.

PI Delcardayre SB, Minshull J, Ness JE, Patten P, Stemmer WPC,

PI Tobin MB;

DR WPI; 98-427565/36.

DR N-PSDB; V44286.

PT Evolution of whole cells and organisms - by recursive DNA sequence

PT recombination in cells to evolve cells having acquired desired

PT function

PS Example 1; Fig 13; 125pp; English.

CC The present invention provides methods employing iterative cycles of

CC recombination and selection/screening for evolution of whole cells

CC and organisms toward acquisition of desired properties, e.g.

CC enhanced recombination, genome copy number, and capacity for

CC expression and/or secretion of proteins and secondary metabolites.

CC The present sequence represents a hyperrecombinogenic variant of a

CC reca protein (see w64213), from an example of the present invention.

SQ Sequence 358 AA;

W64214 Length: 358 April 26, 2000 08:15 Type: P Check: 7100 ..

1 MTGVKWAIDE NKQALRTAL GQIEKQFGKG SIMRLGEDRS MDVETISTGS

51 LSLDIALGAG GLPMGRIVEI YGPESGKTT LTLQVIAAAQ REGKTCAFID

101 AEHALDPIYA RKLGVDIDNL LCSQPDTEQ ALEICDALAR SGADVIVVE

151 SVAALTPKAE IEGEIGDSHM GLAARMMSQA MRKLGNLQK SNTLLIFINQ

201 IRMKIGVMFG NPETTGGNA LKFYASVRLD IRRIGAVKEG ENVVGSETRV

251 KVVKNKIAAP FKQAEFQILY GEGINFYGEL VDLGVKEKLI EKAGAWYSYK

301 GEKIGOGKAN ATAWLKDNPE TAKEIEKKVR ELLLSNPNST PDFSVDDSEG

351 VAETNEDE

! FINDPATTERNS on geneseqp:* allowing 0 mismatches

```

1 1 (I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)PMGRIVEY
    W64215 ck: 6091 len: 358 ! Hyperrecombinogenic variant reca protein cl
      (I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
      (I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEY
46: MDVET
    W64216 ck: 5676 len: 358 ! Hyperrecombinogenic variant reca protein cl
      (I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
      (I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEY
46: MDVET
    W64217 ck: 6188 len: 358 ! Hyperrecombinogenic variant reca protein cl
      (I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
      (I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEY
46: MDVET
    W64218 ck: 6188 len: 358 ! Hyperrecombinogenic variant reca protein cl
      (I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
      (I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEY
46: MDVET
    W64219 ck: 6459 len: 358 ! New minshall reca protein. Evolution of who
      (I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
      (I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEY
46: MDVET
    W64220 ck: 7100 len: 358 ! Hyperrecombinogenic variant reca protein cl
      (I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
      (I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEY
46: MDVET

```

Databases searched:

GeneSeq, Release 36.3, Released on 8Jul1999, Formatted on 9Jul1999

Total finds: 6
Total length: 23,686,106
Total sequences: 188,963
CPU time: 04:02.75

!!AA_SEQUENCE 1.0

ID W64215 standard; Protein: 358 AA.

AC W64215;

DT 28-APR-1999 (first entry)

DE Hyperrecombinogenic variant reca protein clone 4.

KW Escherichia coli: reca protein; hyperrecombinogenic variant; Minshall;

KW recursive sequence recombination; evolution.

OS Escherichia coli.

OS Synthetic.

PN W09831837-A1.

PD 23-JUL-1998.

PF 16-JAN-1998; U00852.

PR 17-JAN-1997; US-035054.

PA (MAXY-) MAXYGEN INC.

PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,

PI Tobin MB;

DR WPI: 98-427565/36.

DR N-PSDB; V44287.

PT Evolution of whole cells and organisms - by recursive DNA sequence
PT recombination in cells to evolve cells having acquired desired
PT function

PS Example 1; Fig 13; 125pp; English.

CC The present invention provides methods employing iterative cycles of
CC recombination and selection/screening for evolution of whole cells
CC and organisms toward acquisition of desired properties, e.g. for
CC enhanced recombinogenicity, genome copy number, and capacity for
CC expression and/or secretion of proteins and secondary metabolites.
CC The present sequence represents a hyperrecombinogenic variant of a
CC reca protein (see w64213), from an example of the present invention.
SQ Sequence 358 AA;

W64215 Length: 358 April 26, 2000 08:16 Type: P Check: 6091

1 MTGVNNAIDE NKQKALAAAL GQIEKQFGKG SIMRLGEDRC MDVETISTGS

51 LSLDIALGAG GLPMDRIVEI YGPESGKTT LTLQVIAAAQ REGKTCAPID

101 AEHALDPIYA RKLGVDDIDL LQSQPDGEG ALEICDALAR SGAVDVIVVE

151 SVAALTPRAE IEGEIGDSHM GLAARMMSQA MRKLGNLQK SNTLLIFNQ

201 IRMKIGVMFG NPETTTGNA LKFYASVRLD IRRIGAVKEG ENNVGSETRV

251 KVVKNKIRAP FKQAEFOILY GEGINFYDEL VDLGVKEKLI EKAGAWISVK

301 GRKVQOGRAN ATAWLKNDPE TAKEIEKKVR ELLLSNPNST PDFSVDDSEB

351 VAETNEDE

!!AA_SEQUENCE 1.0

ID W64216 standard; Protein: 358 AA.

AC W64216;

DT 28-APR-1999 (first entry)

DE Hyperrecombinogenic variant reca protein clone 5.

KW Escherichia coli: reca protein; hyperrecombinogenic variant; Minshall;

KW recursive sequence recombination; evolution.

OS Escherichia coli.

OS Synthetic.

PN W09831837-A1.

PD 23-JUL-1998.

PF 16-JAN-1998; U00852.

PR 17-JAN-1997; US-035054.

PA (MAXY-) MAXYGEN INC.

PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,

PI Tobin MB;

DR WPI: 98-427565/36.

DR N-PSDB; V44288.

PT Evolution of whole cells and organisms - by recursive DNA sequence

PT recombination in cells to evolve cells having acquired desired

PT function

PS Example 1; Fig 13; 125pp; English.

CC The present invention provides methods employing iterative cycles of
CC recombination and selection/screening for evolution of whole cells
CC and organisms toward acquisition of desired properties, e.g.
CC enhanced recombinogenicity, genome copy number, and capacity for
CC expression and/or secretion of proteins and secondary metabolites.

CC The present sequence represents a hyperrecombinogenic variant of a

CC reca protein (see w64213), from an example of the present invention.

SQ Sequence 358 AA;

W64216 Length: 358 April 26, 2000 08:16 Type: P Check: 5676

1 MTGVNNAIDE NKQKALAAAL GQIEKQFGKG SIMRLGEDRS MDVETISTGS

51 LSLDIALGAG GLPMDRIVEI YGPESGKTT LTLQVIAAAQ REGKTCAPID

101 AEHALDPIYA RKLGVDDIDL LQSQPDGEG ALEICDALAR SGAVDVIVVE

151 SVAALTPRAE IEGEIGDSHM GLAARMMSQA MRKLGNLQK SNTLLIFNQ

201 IRMKIGVMFG NPETTTGNA LKFYASVRLD IRRIGAVKEG ENNVGSETRV

251 KVKNKIAAP FQAQEQIILY DGINFYGEL VDLGVKKEKLI EKAGAWYSYK
 301 GERAGOGKAN AAWLKGNP TAKEIEKKVR ELLLSNPST PDFSVDDSEG
 351 VAETNEDE

!!AA_SEQUENCE 1.0
 ID W64217 standard; Protein; 358 AA.
 AC W64217;
 DT 28-APR-1999 (first entry)
 DE Hyperrecombinogenic variant recA protein clone 6.
 KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;
 OS Escherichia coli.
 OS Synthetic.
 PN WO9831837-A1.
 PD 23-JUL-1998.
 PF 16-JAN-1998; U00852.
 PR 17-JAN-1997; US-035054.
 PA (MAXY-) MAXYGEN INC.
 PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,
 PI Tobin MB;
 DR WPI: 98-427565/36.
 DR N-PSDB; V44289.
 PT Evolution of whole cells and organisms - by recursive DNA sequence
 PT recombination in cells to evolve cells having acquired desired
 PT function
 PS Example 1; Fig 13; 125pp; English.
 CC The present invention provides methods employing iterative cycles of
 CC recombination and selection/screening for evolution of whole cells
 CC and organisms toward acquisition of desired properties, e.g.
 CC enhanced recombinogenicity, genome copy number, and capacity for
 CC expression and/or secretion of proteins and secondary metabolites.
 CC The present sequence represents a hyperrecombinogenic variant of a
 CC recA protein (see w64213), from an example of the present invention.
 CC Sequence 358 AA;
 SQ

W64217 Length: 358 April 26, 2000 08:16 Type: P Check: 6188
 1 MTGVKMAIDE NKQKALAAAL GQIEKQFGKG SIMRLGEDRS MDVETISTGS
 51 LSLDIALGAG GLPMGRIVEI YGPSSGKTT LTLOVIAAAQ REGKTCAFID
 101 AEHALDPIYA RKLGVDDIDNL LCSQPDGTGEQ ALEICDALAR SGAVDVIVVE
 151 SVAALTPKAE IEGEIGDSHM GLAARMMSQA MRKLGNLQKQ SNTLLIFINQ
 201 IRMKIGVMFG NPETTTGGNA LKFYASVRLD IRRIGAVKEG ENVVGSETRV
 251 KVKNKIAAP FQAQEQIILY DGINFYGEL VDLGVKKEKLI EKAGAWYSYK
 301 GERAGOGKAN ATAWLKDNP TAKEIEKKVR ELLLSNPST PDFSVDDSEG
 351 VAETNEDE

!!AA_SEQUENCE 1.0
 ID W64218 standard; Protein; 358 AA.
 AC W64218;
 DT 28-APR-1999 (first entry)
 DE Hyperrecombinogenic variant recA protein clone 13.
 KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;
 OS Escherichia coli.
 OS Synthetic.
 PN WO9831837-A1.
 PD 23-JUL-1998.
 PF 16-JAN-1998; U00852.
 PR 17-JAN-1997; US-035054.
 PA (MAXY-) MAXYGEN INC.
 PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,
 PI Tobin MB;
 DR WPI: 98-427565/36.

DR N-PSDB; V44290.
 PT Evolution of whole cells and organisms - by recursive DNA sequence
 PT recombination in cells to evolve cells having acquired desired
 PT function
 PS Example 1; Fig 13; 125pp; English.
 CC The present invention provides methods employing iterative cycles of
 CC recombination and selection/screening for evolution of whole cells
 CC and organisms toward acquisition of desired properties, e.g.
 CC enhanced recombinogenicity, genome copy number, and capacity for
 CC expression and/or secretion of proteins and secondary metabolites.
 CC The present sequence represents a hyperrecombinogenic variant of a
 CC recA protein (see w64213), from an example of the present invention.
 CC Sequence 358 AA;
 SQ

W64218 Length: 358 April 26, 2000 08:16 Type: P Check: 6188

1 MTGVKMAIDE NKQKALAAAL GQIEKQFGKG SIMRLGEDRS MDVETISTGS
 51 LSLDIALGAG GLPMGRIVEI YGPSSGKTT LTLOVIAAAQ REGKTCAFID
 101 AEHALDPIYA RKLGVDDIDNL LCSQPDGTGEQ ALEICDALAR SGAVDVIVVE
 151 SVAALTPKAE IEGEIGDSHM GLAARMMSQA MRKLGNLQKQ SNTLLIFINQ
 201 IRMKIGVMFG NPETTTGGNA LKFYASVRLD IRRIGAVKEG ENVVGSETRV
 251 KVKNKIAAP FQAQEQIILY DGINFYGEL VDLGVKKEKLI EKAGAWYSYK
 301 GERAGOGKAN ATAWLKDNP TAKEIEKKVR ELLLSNPST PDFSVDDSEG
 351 VAETNEDE

!!AA_SEQUENCE 1.0
 ID W64213 standard; Protein; 358 AA.

AC W64213;
 DT 28-APR-1999 (first entry)
 DE New Minshall recA protein.
 KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;
 KW recursive recombination; evolution.
 OS Escherichia coli.
 PN WO9831837-A1.
 PD 23-JUL-1998.
 PF 16-JAN-1998; U00852.
 PR 17-JAN-1997; US-035054.
 PA (MAXY-) MAXYGEN INC.
 PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,
 PI Tobin MB; 98-427565/36.
 DR WPI: 98-427565/36.
 DR N-PSDB; V44285.
 PT Evolution of whole cells and organisms - by recursive DNA sequence
 PT recombination in cells to evolve cells having acquired desired
 PT function
 PS Example 1; Fig 13; 125pp; English.
 CC The present invention provides methods employing iterative cycles of
 CC recombination and selection/screening for evolution of whole cells
 CC and organisms toward acquisition of desired properties, e.g.
 CC enhanced recombinogenicity, genome copy number, and capacity for
 CC expression and/or secretion of proteins and secondary metabolites.
 CC The present sequence represents a wild-type recA protein (designated
 CC new Minshall), from an example of the present invention.
 CC Sequence 358 AA;
 SQ

W64213 Length: 358 April 26, 2000 08:16 Type: P Check: 6469

1 MTGVKMAIDE NKQKALAAAL GQIEKQFGKG SIMRLGEDRS MDVETISTGS
 51 LSLDIALGAG GLPMGRIVEI YGPSSGKTT LTLOVIAAAQ REGKTCAFID
 101 AEHALDPIYA RKLGVDDIDNL LCSQPDGTGEQ ALEICDALAR SGAVDVIVVE
 151 SVAALTPKAE IEGEIGDSHM GLAARMMSQA MRKLGNLQKQ SNTLLIFINQ
 201 IRMKIGVMFG NPETTTGGNA LKFYASVRLD IRRIGAVKEG ENVVGSETRV

251 KVVKNKIAAP FKQAEFQILY GEGINFYGEL VDLGVKKEKLI EKAGAWYSYK
301 GEKIGQGRAN ATAWLKDNPKE TAKEIEKKVR ELLLSNPNST PDFSVDDSEG
351 VAETNEDE

!!AA_SEQUENCE 1.0

ID W64214 standard; Protein; 358 AA.

AC W64214;

DE 28-APR-1999 (first entry)

DE Hyperrecombinogenic variant recA protein clone 2.

KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;

KW recursive sequence recombination; evolution.

OS Escherichia Coli.

OS Synthetic.

WO9831837-A1.

PD 23-JUL-1998.

PF 16-JAN-1998; U00852.

PR 17-JAN-1997; US-035054.

PA (MAXY-) MAXYGEN INC.

PI Delcardayre SB, Minshull J, Ness JE, Patten P, Stemmer WPC,

PI Tobin MB;

DR WPI; 98-427565/36.

DR N-PSDB; V44286.

PT Evolution of whole cells and organisms - by recursive DNA sequence

PT recombination in cells to evolve cells having acquired desired

PT function

PS Example 1; Fig 13; 125pp; English.

CC The present invention provides methods employing iterative cycles of

CC recombination and selection/screening for evolution of whole cells

CC and organisms toward acquisition of desired properties, e.g.

CC enhanced recombination, genome copy number, and capacity for

CC expression and/or secretion of proteins and secondary metabolites.

CC The present sequence represents a hyperrecombinogenic variant of a

CC recA protein (see w64213), from an example of the present invention.

SQ Sequence 358 AA;

W64214 Length: 358 April 26, 2000 08:16 Type: P Check: 7100 ..

1 MTGVKMAIDE NKQALRTAL GQIEKQFGKG SIMRLGEDRS MDVETISTGS

51 LSLDIALGAG GLPMGRIVEI YGPESGKTT LTLQVIAAAQ REGKTCAFID

101 AEHALDPIYA RKLQVDIDNL LCSQPDTEQ ALEICDALAR SGAVDVIVVE

151 SVAALTPKAE IEGEIGDSHM GLAARMMSQA MRKLGNLQK SNTLLIFINQ

201 IRMKIGVMFG NPETTGGNA LKFYASVRD IRRIGAVREG ENVVGSETRV

251 KVVKNKIAAP FKQAEFQILY GEGINFYGEL VDLGVKKEKLI EKAGAWYSYK

301 GEKIGQGRAN ATAWLKDNPKE TAKEIEKKVR ELLLSNPNST PDFSVDDSEG

351 VAETNEDE


```

! FINDPATTERNS on swp:* allowing 0 mismatches
!
1 1 IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)
RECA_ECOLI ck: 8674 len: 352 ! P03017 escherichia coli, and shigella flexn
IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
ISTGSLSDIALGAGGLPMGRIVEIY GPESS
40: MDVET

RECA_ENTAG ck: 7629 len: 354 ! P33037 enterobacter agglomerans. reca prote
IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
ISTGSLSDIALGAGGLPMGRIVEIY GPESS
41: MDVET

RECA_PROVU ck: 9127 len: 325 ! P26346 proteus vulgaris. reca protein. 12/1
IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
ISTGSLSDIALGAGGLPMGRIVEIY GPESS
41: MDVET

RECA_SERMA ck: 5093 len: 354 ! P17479 serratia marcescens. reca protein. 1
IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
ISTGSLSDIALGAGGLPMGRIVEIY GPESS
41: MDVET

RECA_SHISO ck: 8506 len: 352 ! Q9zff6 shigella sonnei. reca protein. 12/19
IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
ISTGSLSDIALGAGGLPMGRIVEIY GPESS
40: MDVET

RECA_XENBV ck: 6641 len: 358 ! P96185 xenorhabdus bovienii. reca protein.
IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
ISTGSLSDIALGAGGLPMGRIVEIY GPESS
41: MDVET

RECA_YERPE ck: 8556 len: 356 ! P37858 yersinia pestis. reca protein. 12/19
IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
ISTGSLSDIALGAGGLPMGRIVEIY GPESS
41: MDVET

Q9X5P5 ck: 4576 len: 358 ! Q9X5P5 xenorhabdus nematophilus. reca prote
IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
ISTGSLSDIALGAGGLPMGRIVEIY GPESS
41: MDVET

Databases searched:
SWISS-PROT, Release 38.1, Released on 20Nov1999, Formatted on 28Dec1999
SPRMBL, Release 12.0, Released on 1Nov1999, Formatted on 27Dec1999

Total finds: 8
Total length: 99,198,988
Total sequences: 308,107
CPU time: 07:02.03

! IAA_SEQUENCE 1.0
ID RECA_ECOLI STANDARD;
AC P03017; P26347; P78213;

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA OR LEXB OR UMUB OR RECH OR RNMB OR TIF OR ZAB.
OS Escherichia coli, and Shigella flexneri.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
[1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-5.
RC SPECIES=E.COLI;
RX MEDLINE; 80145618.
RA HORII T., OGAWA T., OGAWA H.;
RT "Organization of the reca gene of Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:313-317(1980).
[2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-2.
RC SPECIES=E.COLI;
RX MEDLINE; 80234673.
RA SANCAR A., STACHELEK C., KONIGSBERG W., RUPP W.D.;
RT "Sequences of the reca gene and protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:2611-2615(1980).
[3]
RP SEQUENCE FROM N.A.
RC SPECIES=E.COLI, AND S.FLEXNERI; STRAIN=B/R;
RX MEDLINE; 91109725.
RA ZHAO X.J., MCENTEE K.;
RT "DNA sequence analysis of the reca genes from Proteus vulgaris,
RT Erwinia carotovora, Shigella flexneri and Escherichia coli B/r.";
RL Mol. Gen. Genet. 222:369-376(1990).
[4]
RP SEQUENCE FROM N.A.
RC SPECIES=E.COLI; STRAIN=K12 / MG1655;
RX MEDLINE; 97426617.
RA BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RA RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
RA MAU B., SHAO Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
[5]
RP SEQUENCE FROM N.A.
RC SPECIES=E.COLI; STRAIN=K12;
RX MEDLINE; 97349980.
RA YAMAMOTO Y., AIBA H., BABA T., HAYASHI K., INADA T., ISONO K.,
RA ITOH T., KIMURA S., KITAGAWA M., MAKINO K., MIKI T., MITSUHASHI N.,
RA MIZOBUCHI K., MORI H., NAKADE S., NAKAMURA Y., NASHIMOTO H.,
RA OSHIMA T., OYAWA S., SAITO N., SAMPEI G., SATOH Y., SIVASUNDARAM S.,
RA TAGAMI H., TAKAHASHI H., TAKEDA J., TAKEMOTO K., UEHARA K., WADA C.,
RA YAMAGATA S., HORIUCHI T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT - K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
[6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RC SPECIES=E.COLI;
RX MEDLINE; 92114994.
RA STORY R.M., WEBER I.T., STEITZ T.A.;
RT "The structure of the E. coli reca protein monomer and polymer.";
RL Nature 355:318-325(1992).
[7]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE; 97185905.
RA YU X., EGELMAN E.H.;
RT "The RecA hexamer is a structural homologue of ring helicases.";
RL Nat. Struct. Biol. 4:101-104(1997).
[8]
RP ERRATUM.
RC SPECIES=E.COLI;
RA STORY R.M., WEBER I.T., STEITZ T.A.;
RL Nature 355:567-567(1992).
[9]

```

RP STRUCTURE OF ATP-BINDING FOLD.
 RC SPECIES=E.COLI;
 RX MEDLINE: 92115005.
 RA STORY R.M., STEITZ T.A.;
 RL Nature 355:374-376(1992).
 CC 1- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
 CC PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
 CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
 CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
 CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
 CC CLEAVAGE.
 CC 1- INDUCTION: IN RESPONSE TO LOW TEMPERATURE. SENSITIVE TO
 CC TEMPERATURE THROUGH CHANGES IN THE LINKING NUMBER OF THE DNA.
 CC 1- DATABASE: NAME=E.COLI reca Web page;
 CC WWW="http://monera.ncl.ac.uk:80/protein/final/reca.htm".
 CC 1- SIMILARITY: BELONGS TO THE RECA FAMILY.
 CC -----
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 CC -----
 CC EMBL: V00328; CAA23618.1;
 CC EMBL: X55553; CAB56806.1;
 CC EMBL: AE000354; AAC75741.1;
 CC EMBL: D90892; CAB22490.1;
 CC PIR: A03548; ROECA.
 CC PIR: S11931; S11931.
 CC PDB: 1REA; 31-OCT-93.
 CC PDB: 2REB; 31-OCT-93.
 CC PDB: 2REC; 01-APR-97.
 CC PDB: 1AA3; 23-JUL-97.
 CC SWISS-2DPAGE; P03017; COLI.
 CC ECO2DBASE; C039.3; 6TH EDITION.
 CC ECODBASE; EG10823; RECA.
 CC PROSITE: PS00321; RECA.
 CC PFAW; PF00154; reca; 1.
 CC DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding;
 CC 3D-structure.
 CC INIT MET 0 0
 CC NP_BIND 66 73
 CC CONFLICT 112 112
 CC TURN 4 4
 CC HELIX 5 21
 CC TURN 23 25
 CC TURN 29 30
 CC STRAND 39 40
 CC HELIX 45 50
 CC TURN 51 51
 CC STRAND 56 57
 CC TURN 58 59
 CC TURN 61 65
 CC STRAND 68 69
 CC TURN 72 85
 CC TURN 86 87
 CC STRAND 90 94
 CC HELIX 101 106
 CC TURN 107 108
 CC HELIX 111 113
 CC STRAND 115 117
 CC HELIX 122 135
 CC STRAND 140 144
 CC HELIX 146 148
 CC HELIX 152 155
 CC HELIX 166 185
 CC TURN 186 186
 CC TURN 188 193
 CC STRAND 213 218
 CC HELIX 221 233

FT TURN 234 235
 FT STRAND 236 249
 FT STRAND 257 263
 FT TURN 264 266
 FT STRAND 267 268
 FT HELIX 270 280
 FT TURN 281 282
 FT STRAND 285 287
 FT TURN 288 289
 FT STRAND 290 293
 FT TURN 294 295
 FT STRAND 296 300
 FT HELIX 301 311
 FT HELIX 313 327
 SQ SEQUENCE 352 AA; 37842 MW; A6DE5451 CRC32;
 RECA_ECOLI Length: 352 April 26, 2000 08:19 Type: P Check: 8674
 1 AIDENKQKAL AALGQIEKQ FGKGSIMRLG EDRSMDVETI STGSLSLDIA
 51 LGAGGLPWGR IVEIYGPESS GKTTLTLOVI AAQREGKTC AFIDAEHALD
 101 PYARKLQVD IDNLLSQPD TGEQALEICD ALARSGAVDV IVDVSVAAIT
 151 PRAEIEGEIG DSHMGLAARM MSQAMRKLAG NLKQSNLTLLI FINQIRMKIG
 201 VMFGNPEITT GGNALKFYAS VRLDIRRIGA VKEGENVYVGS ETRVKVYKVK
 251 IAAPFKQAEF QILYGEINF YGELVDLGVK EKLIKAGAW YSYKGEKIGQ
 301 GRANATAWLK DNPETAKEIE KKYRELLSN PNSTPDFSVD DSEGVATNE
 351 DF
 !!AA_SEQUENCE 1.0
 ID RECA_ENTAG STANDARD; PRT; 354 AA.
 AC P33037;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE RECA PROTEIN.
 GN RECA.
 OS Enterobacter agglomerans.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Pantoea.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA RAPPOLO C.S.J., KLINGMUELLER W.;
 RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
 CC 1- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
 CC PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
 CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
 CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
 CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
 CC CLEAVAGE.
 CC 1- SIMILARITY: BELONGS TO THE RECA FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L03291; AAA91766.1;
 CC PIR: S31481; S31481.
 CC HSP: P03017; 2REB.
 CC PROSITE: PS00321; RECA; 1.
 CC PFAW: PF00154; reca; 1.
 CC DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
 CC NP_BIND 67 74
 CC SEQUENCE 354 AA; 37898 MW; 629E3B60 CRC32;
 SQ

RECA_ENTAG Length: 354 April 26, 2000 08:19 Type: P Check: 7629

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1 MAIDENKQKA LAAALGQIEK QFGKGSIMRL GEDRSMDET ISTGSLSLDI
51 ALGAGGLPMG RIVEIYGPE SGKTTTLQV IAAAREGKT CAFIDAEHAL
101 DPIYAKKLGV DIDNLLCSOP DTGEQALEIC DALTRSGAVD VIIVDSVAAL
151 TPRAIEGEI GDSHMGGLAAR MMSQAMRKL GNLKNANTLL IFINQIRMKI
201 GVMFGNPETT TGNALKFYA SVRLDIRRG AIKGDGVVVG SETRVKVKVN
251 KIAAPFKQAE FOILYEGIN INGLIDLGV KHKLIKAGA WSYNGEKIG
301 OGRANSCNYL KENPKVAEL DKLRDMLLS GTGELSVATT AEDADDNMET
351 SEEF

!!AA_SEQUENCE 1.0
ID RECA_PROVU STANDARD; PRT; 325 AA.
AC P26346;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91109725.
RA ZHAO X., MCENTEE K.;
RT "DNA sequence analysis of the reca genes from Proteus vulgaris,
RT Erwiniia carotovora, Shigella flexneri and Escherichia coli B/r.";
RL Mol. Gen. Genet. 232:369-376(1990).
CC -|- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE [ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -|- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X5555; ; NOT_ANNOTATED_CDS.
CC DR HSSP; P03017; 2REB.
CC DR PROSITE; PS00321; RECA; 1.
CC DR PFAM; PF00154; reca; 1.
CC KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
CC NP_BIND 67 74 ATP (BY SIMILARITY).
CC SQ SEQUENCE 325 AA; 34790 MW; D46C9851 ORC32;
RECA_PROVU Length: 325 April 26, 2000 08:19 Type: P Check: 9127

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251 KVAAPFKQAE FOILYEGIN INGLVDLGV KHKLIKAGA WSYNGDKIG
301 OGRANACNLF KENSLVKETK NFNGC

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!!AA_SEQUENCE 1.0
ID RECA_SERMA STANDARD; PRT; 354 AA.
AC P17479;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-SM6;
RX MEDLINE; 90094239.
RA BALL T.K., WASMUTH C.R., BRAUNAGEL S.C., BENEDIK M.J.;
RT "Expression of Serratia marcescens extracellular proteins requires
RT reca.";
RL J. Bacteriol. 172:342-349(1990).
CC -|- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -|- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M22935; AAA26567.1; -.
CC DR HSSP; P03017; 2REB.
CC DR PROSITE; PS00321; RECA; 1.
CC DR PFAM; PF00154; reca; 1.
CC KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
CC NP_BIND 67 74 ATP (BY SIMILARITY).
CC SQ SEQUENCE 354 AA; 37909 MW; 2BC62FDE CRC32;
RECA_SERMA Length: 354 April 26, 2000 08:19 Type: P Check: 5093

```

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1 MAIDENKQKA LAAALGQIEK QFGKGSIMRL GEDRSMDET ISTGSLSLDI
51 ALGAGGLPMG RIVEIYGPE SGKTTTLQV IAAAREGKT CAFIDAEHAL
101 DPIYAKKLGV DIDNLLCSOP DTGEQALEIC DALTRSGAVD VIIVDSVAAL
151 TPRAIEGEI GDSHMGGLAAR MMSQAMRKL GNLKNANTLL IFINQIRMKI
201 GVMFGNPETT TGNALKFYA SVRLDIRRG AIKGDGVVVG SETRVKVKVN
251 KIAAPFKQAE FOILYEGIN INGLVDLGV KHKLIKAGA WSYNGEKIG
301 OGRANACNLF KENPAIAEL DKLRDMLLH SGGELVAASG DDFEDDEAET
351 SEQF

!!AA_SEQUENCE 1.0
ID RECA_SHISO STANDARD; PRT; 352 AA.
AC Q9ZFP6;
DT 15-DEC-1999 (Rel. 39, Created)
DT 15-DEC-1999 (Rel. 39, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.

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OS Shigella sonnei.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Shigella.
 RL [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-KNHI104S;
 RA PARK Y.C., SHIN H.J., KIM Y.C.;
 RT "Cloning and nucleotide sequence of the recA gene from Shigella sonnei KNHI04S";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE.
 CC
 CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
 CC
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 CC
 CC EMBL; AF101227; AAC72856.1;
 DR PROSITE; PS00321; RECA; 1.
 KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
 FT INIT_MET 0 BY SIMILARITY.
 FT NP_BIND 66 73 ATP (POTENTIAL).
 FT SEQUENCE 352 AA; 37799 MW; ADB29D96 CRC32;
 SQ
 RECA_SHISO Length: 352 April 26, 2000 08:19 Type: P Check: 8506
 1 AIDENKQKAL AALAQIEKQ FGKGSIMRLG EDRSMDEVETI STGSLSLDIA
 51 LGAGGLPMGR IVEIYGPRESS GKTTLTQVI AALAQEGKTC AFIDAEHALD
 101 PIYARKLGVD IDNLLCSQPD TSGQALEICD ALARSGAVDV IVDVSAALT
 151 PKAEIEGEGT DSHGLAARM MSQAMRKLKGL NLKQSNLLI FINQIRMKIG
 201 VMFGNPETTT GGNALKFYAS VRLDIRRIGA VKEGENVVGES ETRVKVVKNK
 251 IAAPFKQAEF QILYEGGINF YGELVDLGK EXLIEKAGAW YSYGKIGQ
 301 GKANATAWLK DNPETAKEIE KKVRELLSN PNSTPDFSVD DSEGVAEETNE
 351 DF
 A SEQUENCE 1.0
 ID RECA_XENBV STANDARD; PRT; 358 AA.
 AC P96185;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-DEC-1999 (Rel. 39, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE RECA PROTEIN.
 GN RECA.
 OS Xenorhabdus bovienii.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Xenorhabdus.
 RL [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-T228/1;
 RA PINYON R.A., ORMSBY R., RALSTON H., THOMAS C.J.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE.
 CC
 CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
 CC
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 CC
 CC EMBL; AF101227; AAC72856.1;
 DR PROSITE; PS00321; RECA; 1.
 KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
 FT INIT_MET 0 BY SIMILARITY.
 FT NP_BIND 66 73 ATP (POTENTIAL).
 FT SEQUENCE 352 AA; 37799 MW; ADB29D96 CRC32;
 SQ
 RECA_SHISO Length: 352 April 26, 2000 08:19 Type: P Check: 8506
 1 AIDENKQKAL AALAQIEKQ FGKGSIMRLG EDRSMDEVETI STGSLSLDIA
 51 LGAGGLPMGR IVEIYGPRESS GKTTLTQVI AALAQEGKTC AFIDAEHALD
 101 PIYARKLGVD IDNLLCSQPD TSGQALEICD ALARSGAVDV IVDVSAALT
 151 PKAEIEGEGT DSHGLAARM MSQAMRKLKGL NLKQSNLLI FINQIRMKIG
 201 VMFGNPETTT GGNALKFYAS VRLDIRRIGA VKEGENVVGES ETRVKVVKNK
 251 IAAPFKQAEF QILYEGGINF YGELVDLGK EXLIEKAGAW YSYGKIGQ
 301 GKANATAWLK DNPETAKEIE KKVRELLSN PNSTPDFSVD DSEGVAEETNE
 351 DF

CC
 CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
 CC
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 CC
 CC EMBL; U87924; AAD12585.1;
 DR HSP; P03017; 2REB.
 DR PROSITE; PS00321; RECA; 1.
 DR PFAM; PF00154; recA; 1.
 KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
 FT NP_BIND 67 74 ATP (POTENTIAL).
 FT SEQUENCE 358 AA; 38487 MW; 3587853C CRC32;
 SQ
 RECA_XENBV Length: 358 April 26, 2000 08:19 Type: P Check: 6641
 1 MANDENKQKA LAALQIEKQ QFGKGSIMRL GENRSMOVET ISTGSLSLDI
 51 ALGAGGLPMG RIVEIYGPES SGKTTITLQV IASAQREGKT CAFIDAEHAL
 101 DPVYAKKLGV DIDNLLCSQP DTGEQALEIC DALSRSGAVD VIVVDSVAAL
 151 TPKEIEGEI GDSHMGLAAR MMSQAMRKLK GLNKNSTLL IFINQIRMKI
 201 GVMEGNPETT TGNALKFYA SVRLDIRRTG SVKNGDEVYV SETRVKVVKN
 251 KIAAPFKQAE FQILYEGGIN TFGELVDLGK KHKMVERAGA WSYVNGDKIG
 301 QOKANATYIL KEHPEVSAEL DKKLRELLLN NTGGFSSNVS DYVADYEDNG
 351 BEVKNEEF
 A SEQUENCE 1.0
 ID RECA_YERPE STANDARD; PRT; 356 AA.
 AC P37858;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE RECA PROTEIN.
 GN RECA.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Yersinia.
 RL [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-231;
 RA KYUKOV V.M., SUCHKOV I.Y., SAZYKIN I.S., MISHANKIN B.N.;
 RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE.
 CC
 CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
 CC
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 CC
 CC EMBL; X75336; CAA53084.1;
 DR PIR; S37586; S37586.
 DR HSP; P03017; 2REB.
 DR PROSITE; PS00321; RECA; 1.
 DR PFAM; PF00154; recA; 1.

KW DNA damage: DNA recombination; SOS response; ATP-binding; DNA-binding.
FT NP_BIND 67 74 ATP (BY SIMILARITY).
SQ SEQUENCE 356 AA; 37912 MW; 60B356BF CRC32;

RECA_YERPE Length: 356 April 26, 2000 08:19 Type: P Check: 8556 ..

1 MAIDENKOKA LAAALGQIEK QFGKGSIMRL GEDRSMDVET ISTGSLSLDI
51 ALGAGGLPMG RIVEIYGPEP SGKTTLTQV IAAAQREGKT CAFIDAEHAL
101 DPIYAKKLGV DIDNLLCSQP DTGEQALEIC DALTRSGAVD VIIVDSVAAL
151 TPKAEIEGEI GDSHMGAAAR MMSQAMRKLA GNKKNANTLL IFINQIRMKI
201 GVMFGNPETP TGGNALKFYA SVRLDIRRTG AVKGDGVVVG SETRVKVKVN
251 KIAAPFKQAE FQIILYEGIN INGELVDLGV KKLIEKAGA WYSYVGDKIG
301 QOKANASNYL KENPANAEL DKKLREMLN GNGEQPVAA ATAEFADGAD
351 ETNEEF

!!AA_SEQUENCE 1.0

ID Q9XSP5 PRELIMINARY; PRT; 358 AA.

AC Q9XSP5;

DT 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)

DE RECA PROTEIN.

GN RECA.

OS Xenorhabdus nematophilus.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Xenorhabdus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-AN6;

RA HEW F.H., THOMAS C.J.;

RT "Analysis of the Xenorhabdus nematophilus AN6 recA gene sequence.";

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

CC FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE

CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF

CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT

CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS

CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC

CC CLEAVAGE.

EMBL; AF127333; RAD32599.1; ..

DR PROSITE; PS00321; RECA; 1.

KW DNA damage: DNA recombination; SOS response; ATP-binding; DNA-binding.

SQ SEQUENCE 358 AA; 38586 MW; 51984C91 CRC32;

Q9XSP5 Length: 358 April 26, 2000 08:19 Type: P Check: 4576 ..

1 MANDENKOKA LAAALGQIEK QFGKGSIMRL GENRSMDVET ISTGSLSLDI

51 ALGAGGLPMG RIVEIYGPEP SGKTTLTQV IAAAQREGRT CAFIDAEHAL

101 DVIYAKKLGV DIDNLLCSQP DTGEQALEIC DALSRSGAVD VIIVDSVAAL

151 TPKAEIEGEI GDSHMGAAAR MMSQAMRKLA GNKKNANTLL IFINQIRMKI

201 GVMFGNPETP PGGNALKFYA SVRLDIRRTG SVKNGDEVVG SETRVKVKVN

251 KYAAPFKQAE FQIILYEGIN TLGELIDLV KHKWEEKAGA WYSYNGDKIG

301 QOKANATIYL KEHPETAEL NKKLRDLLH NTGDFSSAAS DYVTYEDNT

351 EEVNEEF

WQSRH (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 25 12:28:13 2000; MasPar time 43.83 seconds
41.128 Million cell updates/sec

Tabular output not generated.

Title: >seqimod
Description: (1-26) from 103.pep
Perfect Score: 140
Sequence: 1 ISTXSLSLDIALXXXLPMXRIIVEY 26

Scoring table: PAM 150
Gap 15

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl12
1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified
13:sp-vertebrate 14:sp-virus

Statistics: Mean 29.804; Variance 47.930; scale 0.622

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	140	100.0	358	2	Q9X5P5 RECA PROTEIN.	2.73e-14
2	124	88.6	363	2	Q9XBC1 RECA PROTEIN.	7.02e-11
3	122	87.1	339	2	Q9X5D8 RECA PROTEIN.	1.84e-10
4	115	82.1	131	2	O05556 RECA.	5.16e-09
5	113	80.7	347	2	Q92MS7 RECA PROTEIN.	1.37e-08
6	111	79.3	376	10	Q92UP2 RECA PROTEIN.	3.37e-08
7	108	77.1	119	2	O31058 RECA (FRAGMENT).	1.36e-07
8	108	77.1	237	2	O86402 RECA PROTEIN (FRAGMENT)	1.36e-07
9	108	77.1	237	2	O86150 RECA PROTEIN (FRAGMENT)	1.36e-07
10	106	75.7	352	2	O84556 RECA PROTEIN.	8.22e-06
11	99	70.7	237	2	O86384 RECA PROTEIN (FRAGMENT)	4.33e-04
12	90	64.3	319	2	O60057 RECA-LIKE PROTEIN.	1.46e-01
13	76	54.3	130	2	Q53854 NITRATE ABC TRANSPORT	3.22e-01
14	74	52.9	244	1	O30150 CHALCONE SYNTHASE-LIKE	7.02e-01
15	72	51.4	389	10	O23811 Y22 PROTEIN.	7.02e-01
16	72	51.4	389	10	O23811 Y22 PROTEIN.	7.02e-01
17	67	47.9	701	2	O51403 NA+/H+ ANTIPOTER (NAP	4.65e+00
18	66	47.1	541	4	O94941 KIAA0860 PROTEIN.	6.72e+00
19	65	46.4	133	4	O15292 HCAT-2B (FRAGMENT).	9.69e+00
20	65	46.4	173	6	O02806 HIGH AFFINITY CATIONIC	9.69e+00

21	65	45.4	261	11	Q62971	RCAT2 (FRAGMENT).	9.68e+00
22	64	45.7	244	2	P73818	HYPOTHETICAL 27.5 KD P	1.39e+01
23	64	45.7	277	8	O79317	HYPOTHETICAL 31.7 KD P	1.39e+01
24	64	45.7	277	8	O79334	HYPOTHETICAL 31.7 KD P	1.39e+01
25	64	45.7	277	8	O79381	HYPOTHETICAL 31.7 KD P	1.39e+01
26	64	45.7	277	8	O79543	HYPOTHETICAL 31.8 KD P	1.39e+01
27	64	45.7	277	8	O79353	HYPOTHETICAL 31.8 KD P	1.39e+01
28	64	45.7	277	8	O79975	HYPOTHETICAL 31.7 KD P	1.39e+01
29	64	45.7	277	8	O79366	HYPOTHETICAL 31.8 KD P	1.39e+01
30	64	45.7	279	8	O79459	HYPOTHETICAL 32.1 KD P	1.39e+01
31	64	45.7	279	8	O79345	HYPOTHETICAL 32.0 KD P	1.39e+01
32	64	45.7	279	8	O79339	HYPOTHETICAL 32.0 KD P	1.39e+01
33	64	45.7	279	8	O79348	HYPOTHETICAL 31.9 KD P	1.39e+01
34	64	45.7	279	8	O79541	HYPOTHETICAL 32.3 KD P	1.39e+01
35	64	45.7	279	8	O79941	HYPOTHETICAL 32.0 KD P	1.39e+01
36	64	45.7	280	8	O79343	HYPOTHETICAL 32.1 KD P	1.39e+01
37	64	45.7	291	8	O79309	HYPOTHETICAL 33.5 KD P	1.39e+01
38	63	45.0	105	1	O28815	HYPOTHETICAL 12.4 KD P	1.98e+01
39	63	45.0	225	5	O96702	SODIUM PROTON ANTIPO	1.98e+01
40	63	45.0	329	6	O28536	CATIONIC AMINO ACID TR	1.98e+01
41	63	45.0	406	1	O54309	ALCOHOL DEHYDROGENASE.	1.98e+01
42	63	45.0	619	11	O08812	CATIONIC AMINO ACID TR	1.98e+01
43	63	45.0	624	11	P70608	CATIONIC AMINO ACID TR	1.98e+01
44	63	45.0	628	11	Q921G1	ECOTROPIC MURINE RETRO	1.98e+01
45	62	44.3	328	11	Q60458	CATIONIC AMINO ACID TR	2.82e+01

ALIGNMENTS

RESULT 1
ID Q9X5P5 PRELIMINARY; PRT; 358 AA.
AC Q9X5P5;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE RECA PROTEIN.
GN RECA.

OS Xenorhabdus nematophilus.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Xenorhabdus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ANG;
RA HEW F.H., THOMAS C.J.;
RT "Analysis of the xenorhabdus nematophilus AN6 recA gene sequence.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.

DR EMBL; AF127333; AAD32599.1; -
DR PROSITE; PS00321; RECA; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
SQ SEQUENCE 358 AA; 38586 MW; 51984C91 CRC32;

Query Match 100.0%; Score 140; DB 2; Length 358;
Best Local Similarity 76.9%; Pred. No. 2.73e-14;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 41 ISTXSLSLDIALGAGGLPMXRIIVEY 66
Qy 1 ISTXSLSLDIALXXXLPMXRIIVEY 26
||| ||||| ||| |||||

RESULT 2
ID Q9XBC1 PRELIMINARY; PRT; 363 AA.
AC Q9XBC1;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE RECA PROTEIN.

GN RECA
OS Rhodopseudomonas palustris.
OC Bacteria; Proteobacteria; alpha subdivision; Bradyrhizobium group;
OC Rhodopseudomonas.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NO. 7.
RX MEDLINE; 99303337.
RA DUMAY V., INUI M., YUKAWA H.;
RT "Molecular analysis of the recA gene and SOS box of the purple non-
sulfur bacterium Rhodopseudomonas palustris no. 7";
RL Microbiology 145:1275-1285(1999).
CC -1- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CLEAVAGE.
DR EMBL; D84467; BAA78779.1; -.
DR PROSITE; PS00321; RECA; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
SQ SEQUENCE 363 AA; 38865 MW; 81D3B0ED CRC32;
Query Match 88.6%; Score 124; DB 2; Length 363;
Best Local Similarity 65.4%; Pred. No. 7.02e-11;
Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Db 52 ISSGSLGDLTALGGLPKRIVEY 77
||:||||| ||:|||||
QY 1 ISTXSLDLIALXXXLPMXRIEY 26
RESULT 3
ID Q9X5D8 PRELIMINARY; PRT; 339 AA.
AC Q9X5D8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Zymomonas mobilis.
OC Bacteria; Proteobacteria; alpha subdivision; Zymomonas group;
OC Zymomonas.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ZM4;
RA LEE H.J., KANG H.S.;
RT "Sequence analysis of 43D2 fosmid clone of Zymomonas mobilis ZM4";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CLEAVAGE.
DR EMBL; AF124757; AAD29645.1; -.
DR PROSITE; PS00321; RECA; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
SQ SEQUENCE 339 AA; 36807 MW; 21492B84 CRC32;
Query Match 87.1%; Score 122; DB 2; Length 339;
Best Local Similarity 65.4%; Pred. No. 1.84e-10;
Matches 17; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
Db 37 ISSGSLGDLTALGGLPKRIVEY 62
||:||||| ||:|||||
QY 1 ISTXSLDLIALXXXLPMXRIEY 26
RESULT 4
ID O05556 PRELIMINARY; PRT; 131 AA.
AC O05556;
RT 01-JUL-1997 (TrEMBLrel. 04, Created)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DE RECA.
GN Mycobacterium leprae.
OS Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
RN [1]
RP SEQUENCE FROM N.A.
RC BADOCK K., CHURCHER C.M.;
RT Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RL [2]
RA BARRELL B.G., RAJANDREAM M.A.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93188700.
RA EIGLMEIER K., HONORE N., WOODS S.A., CAUDRON B., COLE S.T.;
RT "Use of an ordered cosmid library to deduce the genomic organization
of Mycobacterium leprae";
RL Mol. Microbiol. 7:197-206(1993).
DR EMBL; Z94723; CAB08125.1; -.
DR HSSP; P03017; 2REB.
DR PFAM; PF00154; RECA; 1.
SQ SEQUENCE 131 AA; 13616 MW; 18ECEB05 CRC32;
Query Match 82.1%; Score 115; DB 2; Length 131;
Best Local Similarity 57.7%; Pred. No. 5.16e-09;
Matches 15; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
Db 41 IPTGSIALDVALGIGLPRGRIEY 66
||:||||| ||:|||||
QY 1 ISTXSLDLIALXXXLPMXRIEY 26
RESULT 5
ID Q9ZMS7 PRELIMINARY; PRT; 347 AA.
AC Q9ZMS7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Helicobacter pylori J99.
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-J99;
RX MEDLINE; 99120557.
RA ALM R.A., LING L.-S.L., MOIR D.T., KING B.L., BROWN E.D., DOIG P.C.;
RA SMITH D.R., NOONAN B., GUILD B.C., DEJONGE B.L., CARMEL G.;
RA TUMMINO P.J., CARUSO A., URITA-NICKELSEN M., MILLS D.M., IVES C.;
RA GIBSON R., MERBERG D., MILLS S.D., JIANG Q., TAYLOR D.E., VOVIS G.F.,
RA TRUST T.J.;
RT "Genomic-sequence comparison of two unrelated isolates of the human
gastric pathogen Helicobacter pylori";
RL Nature 397:176-180(1999).
CC -1- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CLEAVAGE.
DR EMBL; AE001453; AAD05722.1; -.
DR HSSP; P03017; 2REB.
DR PROSITE; PS00321; RECA; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding;
KW DNA-binding.
SQ SEQUENCE 347 AA; 37623 MW; 7812DC30 CRC32;
Query Match 80.7%; Score 113; DB 2; Length 347;

AC	08B150;	
DT	01-NOV-1998	(TReMBLrel. 08, Created)
DT	01-NOV-1998	(TReMBLrel. 08, Last sequence update)
DT	01-NOV-1999	(TReMBLrel. 12, Last annotation update)
DT	RECA	PROTEIN (FRAGMENT).
DT	RECA.	
OS	Neisseria lactamica.	
OS	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.	
CC	[1]	SEQUENCE FROM N.A.
CC	STRAIN-CCUC 7757, NCTC 10618, LCDC 80-111, LCDC 845;	
CC	SMITH N.H., DONOVAN G.M., CARPENTER A., SPRATT B.G.;	
CC	"Do sexual bacteria have species?";	
CC	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.	
CC	-!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE	
CC	PRESENCE OF SINGLE-STRANDED DNA.	
CC	PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF	
CC	SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT	
CC	HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS	
CC	WITH HEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC	
CC	CLEAVAGE.	
CC		
CC	EMBL; AJ223866; CAA11597.1; -	
CC	EMBL; AJ223863; CAA11594.1; -	

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DR EMBL; AJ223864; CAAL1595.1; -
DR EMBL; AJ223865; CAAL1596.1; -
DR HSSP; P03017; 2REB.
DR PROSITE; PS00321; RECA; 1.
DR PFAM; PF00154; reca; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
FT NON_TER 237 237
FT NON_TER 1
SQ SEQUENCE 237 AA; 25464 MW; B67CDB68 CRC32;

Query Match 77.1%; Score 108; DB 2; Length 237;
Best Local Similarity 60.0%; Pred. No. 1.36e-07;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Db 1 STGSLGDLALGVGGLPRGRIVEIF 25
   |||:||||:|
QY 2 STXSLSLDIALXXXXLPMXRIVEIY 26

RESULT 10
ID 084656 PRELIMINARY; PRT; 352 AA.
O84656
01-NOV-1998 (TRENBLrel. 08, Created)
01-NOV-1998 (TRENBLrel. 08, Last sequence update)
01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE RECA PROTEIN.
CN RECA
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-D/UW-3/CX.
RA STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
RA MITCHELL W.P., OLINGER L., TATSOV R.L., ZHAO Q., KOONIN E.V.,
RA DAVIS R.W.;
RT "Genome Sequence of an Obligate Intracellular Pathogen of Humans:
RT Chlamydia trachomatis.";
RL Science 0:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-D/UW-3/CX.
RA STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
RA MITCHELL W.P., OLINGER L., TATSOV R.L., ZHAO Q., KOONIN E.V.,
RA DAVIS R.W.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC SINGLE-STRANDED DNA BY DUPLEX DNA, THE ATP-DEPENDENT UPTAKE OF
CC PRESENCE OF SINGLE-STRANDED DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
DR EMBL; AE001335; AAC68827.1; -
DR HSSP; P03017; 2REB.
DR PROSITE; PS00321; RECA; 1.
DR PFAM; PF00154; reca; 1.
DR PRINTS; PR00142; RECA.
KW Hypothetical protein; DNA damage; DNA recombination; SOS response;
KW ATP-binding; DNA-binding.
SQ SEQUENCE 352 AA; 37830 MW; D4B5CCD3 CRC32;

Query Match 75.7%; Score 106; DB 2; Length 352;
Best Local Similarity 53.8%; Pred. No. 3.42e-07;
Matches 14; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Db 41 IKTGALSGLDIALGIGVPGKGRIVEIF 66
   |||:||||:|
QY 1 ISTXSLSLDIALXXXXLPMXRIVEIY 26

RESULT 11
ID 086384 PRELIMINARY; PRT; 237 AA.
AC 086384
DE 01-NOV-1998 (TRENBLrel. 08, Created)

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DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE RECA PROTEIN (FRAGMENT).
CN RECA.
OS Neisseria flava.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BANGOR 9.
RA SMITH N.H., DONOVAN G.M., CARPENTER A., SPRATT B.G.;
RT "Do sexual bacteria have species?";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
DR EMBL; AJ223873; CAAL1604.1; -
DR HSSP; P03017; 2REB.
DR PROSITE; PS00321; RECA; 1.
DR PFAM; PF00154; reca; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
FT NON_TER 237 237
FT NON_TER 1
SQ SEQUENCE 237 AA; 25461 MW; 2A50CC00 CRC32;

Query Match 70.7%; Score 99; DB 2; Length 237;
Best Local Similarity 52.0%; Pred. No. 8.22e-06;
Matches 13; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Db 1 STGSLGVDLALGVGGLPRGRIVEIF 25
   |||:||||:|
QY 2 STXSLSLDIALXXXXLPMXRIVEIY 26

RESULT 12
ID Q60057 PRELIMINARY; PRT; 319 AA.
AC Q60057
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE RECA PROTEIN (FRAGMENT).
OS Unknown prokaryotic organism.
OC Bacteria; environmental samples.
RN [1]
RP SEQUENCE FROM N.A.
RA BORCHELLINI P., ANGULO J., DEVORET R., BERTOLOTI R.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
DR EMBL; U20900; AAA62510.1; -
DR HSSP; P03017; 2REB.
DR PROSITE; PS00321; RECA; 1.
DR PFAM; PF00154; reca; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding;
KW DNA-binding.
FT NON_TER 319 319
FT NON_TER 1
SQ SEQUENCE 319 AA; 34041 MW; 507C1D67 CRC32;

Query Match 64.3%; Score 90; DB 2; Length 319;
Best Local Similarity 44.0%; Pred. No. 4.33e-04;
Matches 11; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Db 54 PSGSVKLDLALGVGGLPRGRIVEIY 78
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QY 2 STXSLSLDIALXXXXLPMXRIVEIY 26

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Db      62 VYSLALALSVALPAGILSRERVD 85
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Qy      1 ISTXSLSDIALXXXLPMXRIVE 24

RESULT 15
ID      Q43595          PRELIMINARY;      PRT;    389 AA.
AC      Q43595;
DT      01-NOV-1996 (T=EMBLrel. 01, Created)
DT      01-NOV-1996 (T=EMBLrel. 01, Last sequence update)
DT      01-NOV-1999 (T=EMBLrel. 12, Last annotation update)
DE      CHALCONE SYNTHASE-LIKE.
GN      CHSLK.
OS      Oryza sativa (Rice).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      euryhalophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
OC      Poaceae; Oryza.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C.V. ZHONGHUA 10; TISSUE=FLOWER;
RA      ZHANG Y., QU L., XIE M., GU H., CHEN Z.;
RL      Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
DR      ENBL; X91811; CAA62921.1; -
DR      MENDEL; I5115; Orysa.i193; i5115.
DR      PRAM; PF00195; Chal_stil_synt; 1.
SQ      SEQUENCE 389 AA; 42380 MW; 96F16D84 CRC32;

Query Match           51.4%; Score 72; DB 10; Length 389;
Best Local Similarity 38.1%; Pred.No. 7.02e-01;
Matches              8; Conservative 4; Mismatches 9; Indels 0; Gap

Db      27 LALGKGLEQOVLPOEKVVETY 47
       : : | : | | : | : | : | : |
Qy      6 LSDIALXXXLPMXRIVEIY 26

Search completed: Tue Apr 25 12:30:04 2000
Job time : 111 secs.
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! FINDPATTERNS on swp:* allowing 0 mismatches

1 1 (I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)PMGRIVEIY

RECA_ECOLI ck: 8674 len: 352 1 P03017 escherichia coli, and shigella flexneri
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
(I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
40: MDVET ISTGSLSLDIALGAGGLPMGRIVEIY

RECA_ENTAG ck: 7629 len: 354 1 P33037 enterobacter agglomerans. reca protease
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
(I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
41: MDVET ISTGSLSLDIALGAGGLPMGRIVEIY

RECA_PROVU ck: 9127 len: 325 1 P36346 proteus vulgaris. reca protein. 12/1
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
(I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
41: MDVET ISTGSLSLDIALGAGGLPMGRIVEIY

RECA_SERMA ck: 5093 len: 354 1 P17479 serratia marcescens. reca protein. 1
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
(I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
41: MDVET ISTGSLSLDIALGAGGLPMGRIVEIY

RECA_SHISO ck: 8506 len: 352 1 Q92ff6 shigella sonnei. reca protein. 12/19
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
(I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
40: MDVET ISTGSLSLDIALGAGGLPMGRIVEIY

RECA_XENBV ck: 6641 len: 358 1 P96185 xenorhabdus bovienii. reca protein.
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
(I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
41: MDVET ISTGSLSLDIALGAGGLPMGRIVEIY

RECA_YERPE ck: 8556 len: 356 1 P37858 yersinia pestis. reca protein. 12/19
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
(I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
41: MDVET ISTGSLSLDIALGAGGLPMGRIVEIY

Q9X5P5 ck: 4576 len: 358 1 Q9x5p5 xenorhabdus nematophilus. reca protease
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
(I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
41: MDVET ISTGSLSLDIALGAGGLPMGRIVEIY

Databases searched:

SWISS-PROT, Release 38.1, Released on 20Nov1999, Formatted on 28Dec1999
SPTRMBL, Release 12.0, Released on 1Nov1999, Formatted on 27Dec1999

Total finds: 8
Total length: 99,198,988
Total sequences: 308,107
CPU time: 14:31:00

!!AA_SEQUENCE 1.0
ID RECA_ECOLI
AC P03017; P26347; P78213; PRT; 352 AA.

21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
RECA OR LEXB OR UMUB OR RECH OR RNMB OR TIF OR ZAB.
Escherichia coli, and Shigella flexneri.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
[1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-5.
RC SPECIES-E.COLI;
RX MEDLINE; 80145618.
RA HORII T., OGAWA T., OGAWA H.;
RT "Organization of the reca gene of Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 77:313-317(1980).
[2]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-2.
RC SPECIES-E.COLI;
RX MEDLINE; 80234673.
RA SANCAR A., STACHELEK C., KONIGSBERG W., RUPP W.D.;
RT "Sequences of the reca gene and protein.";
Proc. Natl. Acad. Sci. U.S.A. 77:2611-2615(1980).
[3]
RN SEQUENCE FROM N.A.
RC SPECIES-E.COLI, AND S.FLEXNERI; STRAIN-B/R;
RX MEDLINE; 91109725.
RA ZHAO X.J., MCENTEE K.;
RT "DNA sequence analysis of the reca genes from Proteus vulgaris,
Erwinia carotovora, Shigella flexneri and Escherichia coli B/r.";
Mol. Gen. Genet. 222:369-376(1990).
[4]
RN SEQUENCE FROM N.A.
RC SPECIES-E.COLI;
RX MEDLINE; 97428617.
RA BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
[5]
RN SEQUENCE FROM N.A.
RC SPECIES-E.COLI; STRAIN-K12 / MG1655;
RX MEDLINE; 97349980.
RA YAMAMOTO Y., AIBA H., BABA T., HAYASHI K., INADA T., ISONO K.,
ITO T., KIMURA S., KITAGAWA M., MAKINO K., MIKI T., MITSUHASHI N.,
MIZOBUCHI K., MORI H., NAKADE S., NAKAMURA Y., NASHIMOTO H.,
OSHIMA T., OYAMA S., SAITO N., SAMPEI G., SATOH Y., SIVASUNDARAM S.,
TAGAMI H., TAKAHASHI H., TAKEDA J., TAKEMOTO K., UEHARA K., WADA C.,
YAMAGATA S., HORTUCHI T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
K-12 genome corresponding to 50.0-66.8 min on the linkage map and
analysis of its sequence features.";
DNA Res. 4:191-113(1997).
[6]
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RC SPECIES-E.COLI;
RX MEDLINE; 92114994.
RA STORY R.M., WEBER I.T., STEITZ T.A.;
RT "The structure of the E. coli reca protein monomer and polymer.";
Nature 355:318-325(1992).
[7]
RN X-RAY CRYSTALLOGRAPHY.
RX MEDLINE; 97185905.
RA YU X., EGELMAN E.H.;
RT "The RecA hexamer is a structural homologue of ring helicases.";
Nat. Struct. Biol. 4:101-104(1997).
[8]
RN ERRATUM.
RC SPECIES-E.COLI;
RX STORY R.M., WEBER I.T., STEITZ T.A.;
RL Nature 355:567-567(1992).
[9]

```
RP STRUCTURE OF ATP-BINDING FOLD.
RC SPECIES-E.COLI;
RX MEDLINE; 92115005.
RA STORY R.M., STEITZ T.A.;
RT "Structure of the recA protein-ADP complex.";
RL Nature 355:374-376(1992).
CC -|- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -|- INDUCTION: IN RESPONSE TO LOW TEMPERATURE. SENSITIVE TO
CC TEMPERATURE THROUGH CHANGES IN THE LINKING NUMBER OF THE DNA.
CC -|- DATABASE: NAME-E.coli recA web page;
CC WWW="http://monera.nci.ac.uk:80/protein/final/recA.htm".
CC -|- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC -----
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CC -----
CC EMBL; V00328; CAA23618.1; -.
CC EMBL; X55553; CAB56806.1; -.
CC EMBL; AE000354; AAC75741.1; -.
CC EMBL; D90892; CAB22490.1; -.
CC PIR; A03548; ROECA.
CC PIR; S11931; S11931.
CC PDB; 1REA; 31-OCT-93.
CC PDB; 2REB; 31-OCT-93.
CC PDB; 2REC; 01-APR-97.
CC PDB; 1AA3; 23-JUL-97.
CC SWISS-2DPAGE; P03017; COLI.
CC ECODBASE; C039.3; 6TH EDITION.
CC ECOGENE; EG10823; RECA.
CC PROSITE; PS00321; RECA; 1.
CC PFW; PF00154; recA; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding;
KW 3D-structure.
FT INIT MET 0 0
FT NP_BIND 66 73 ATP.
FT CONFLICT 112 112 D -> E (IN REF. 5).
FT TURN 4 4
FT HELIX 5 21
FT TURN 23 25
FT TURN 29 30
FT STRAND 39 40
FT HELIX 45 50
FT TURN 51 51
FT STRAND 56 57
FT TURN 58 59
FT STRAND 61 65
FT TURN 68 69
FT HELIX 72 85
FT TURN 86 87
FT STRAND 90 94
FT HELIX 101 106
FT TURN 107 108
FT HELIX 111 113
FT STRAND 115 117
FT HELIX 122 125
FT STRAND 140 144
FT HELIX 146 148
FT HELIX 152 155
FT HELIX 166 185
FT TURN 186 186
FT TURN 188 193
FT STRAND 223 228
FT HELIX 221 233
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FT TURN 234 235
FT STRAND 236 249
FT STRAND 257 263
FT TURN 264 266
FT STRAND 267 268
FT HELIX 270 280
FT TURN 281 282
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FT TURN 288 289
FT STRAND 290 293
FT TURN 294 295
FT STRAND 296 300
FT HELIX 301 311
FT HELIX 313 327
SQ SEQUENCE 352 AA; 37842 MW; A6DE5451 CRC32;
RECA_ECOLI Length: 352 April 26, 2000 08:21 Type: P Check: 8674
1 AIDENKQKAL AALGQIEKQ FGKGSIMRLG EDRSMVETI STGSLSLDIA
51 LGAGGLPMGR IVEIYGESS GKTTLTQVI AAQREGKTC AFIDAHAHALD
101 PIYARKLQVD IDNLLCSQPD TGEQALEICD ALARSGADV IVVDSVAALT
151 PKAEIEGEIG DSHMGLAARM MSQAMRKLKGL NLKOSNTLLI FINQIRKKG
201 VMFCNPETTT GGNALKFYAS VRLDIRRIGA VKEGENVVGS ETRVKVVKNK
251 IAAFPKQAEF QIILYGEINP YGELYDLGVK EKLIEKAGAW YSYKGEKIGQ
301 GKANATAWLK DNPETAKEIE KKVRELLLSN PNSTPDFSVD DSEGVATNE
351 DF
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ID RECA_SEQUENCE 1.0 STANDARD; PRT; 354 AA.
AC P33037;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Enterobacter agglomerans.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pantoea.
[1]
RP SEQUENCE FROM N.A.
RA RAPPOLD C.S.J., KLINGMUELLER W.;
RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -|- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L03291; AAA91766.1; -.
CC PIR; S31481; S31481.
CC HSSP; P03017; 2REB.
CC PROSITE; PS00321; RECA; 1.
CC PFW; PF00154; recA; 1.
CC DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
CC NP_BIND 67 74 ATP (BY SIMILARITY).
CC SEQUENCE 354 AA; 37898 MW; 629E3B60 CRC32;
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RECA_ENTAG Length: 354 April 26, 2000 08:21 Type: P Check: 7629

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1 MAIDENKOKA LAAALGQIEK QFGKGSIMRL GEDRSMDET ISTGSLSLDI
51 ALGAGGLPMG RIVEIYGPE SGKTTTLQV IAAAREGKT CAFIDAEHAL
101 DPIYAKKLGVDIDNLLCSQ DTGEQALEIC DALTRSGAVD VIIVDSVAAL
151 TPKAIEGEI GDSHGLAAR MMSQAMRCLA GNKKNANTLL IFINQIRMKI
201 GVMFGNPETT TGGNALKFYA SVRLDIRRIG AIKEDGVVVG SETRVKVVKN
251 KIAAPFKQAE FOILYGEIN INGELIDLGV KHKLIKAKA WYSYNGEKIG
301 OKKANSNYL KENPVAEL DKLRDMLLS GTGELSVAIT AEDADDNMET
351 SEEF

!!IAA_SEQUENCE 1.0
ID RECA_PROVU STANDARD; PRT; 325 AA.
AC P26346;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91109725.
RA ZHAO X., MCENTEE K.;
RT "DNA sequence analysis of the recA genes from Proteus vulgaris,
RT Erwinia carotovora, Shigella flexneri and Escherichia coli B/r.";
RL Mol. Genet. 222:369-376(1990).
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC -----
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CC -----
CC EMBL; X55555; -; NOT_ANNOTATED_CDS.
CC HSP; P03017; 2REB.
CC PROSITE; P500321; RECA; 1.
CC PFAM; PF00154; recA; 1.
CC DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
CC NP_BIND 67 74 ATP (BY SIMILARITY).
CC SEQUENCE 325 AA; 34790 MW; D46C9851 CRC32;
```

RECA_PROVU Length: 325 April 26, 2000 08:21 Type: P Check: 9127

```
1 MAIDENKOKA LAAALGQIEK QFGKGSIMRL GEDRSMDET ISTGSLSLDI
51 ALGAGGLPMG RIVEIYGPE SGKTTTLQV IAAAREGKT CAFIDAEHAL
101 DPIYAKKLGVDIDNLLCSQ DTGEQALEIC DALTRSGAVD VIIVDSVAAL
151 TPKAIEGEI GDSHGLAAR MMSQAMRCLA GNKKNANTLL IFINQIRMKI
201 GVMFGNPETT TGGNALKFYA SVRLDIRRIG AIKEDGVVVG SETRVKVVKN
```

```
251 KVAAPFKQAE FOILYGEIN INGELVDLGV KHKLIKAKA WYSYNGDKIG
301 OKKANACNFL KENSLVKETK NFNGC
```

```
!!IAA_SEQUENCE 1.0
ID RECA_SERMA STANDARD; PRT; 354 AA.
AC P17479;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90094239.
RA BALL T.K., WASMUTH C.R., BRAUNAGEL S.C., BENEDIK M.J.;
RT "Expression of Serratia marcescens extracellular proteins requires
RT recA.";
RL J. Bacteriol. 172:342-349(1990).
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M22935; AAA26567.1; -
CC HSP; P03017; 2REB.
CC PROSITE; P500321; RECA; 1.
CC PFAM; PF00154; recA; 1.
CC DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
CC NP_BIND 67 74 ATP (BY SIMILARITY).
CC SEQUENCE 354 AA; 37909 MW; 2BC62FDE CRC32;
```

RECA_SERMA Length: 354 April 26, 2000 08:21 Type: P Check: 5093

```
1 MAIDENKOKA LAAALGQIEK QFGKGSIMRL GEDRSMDET ISTGSLSLDI
51 ALGAGGLPMG RIVEIYGPE SGKTTTLQV IAAAREGKT CAFIDAEHAL
```

```
101 DPIYAKKLGVDIDNLLCSQ DTGEQALEIC DALTRSGAVD VIIVDSVAAL
```

```
151 TPKAIEGEI GDSHGLAAR MMSQAMRCLA GNKKNANTLL IFINQIRMKI
```

```
201 GVMFGNPETT TGGNALKFYA SVRLDIRRIG AIKEDGVVVG SETRVKVVKN
```

```
251 KIAAPFKQAE FOILYGEIN INGELVDLGV KHKLIKAKA WYSYNGEKIG
```

```
301 OKKANACNFL KENPATAAEL DKLRDLLLH SGGELVAAASG DDFEDDEAET
```

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351 SEQF
```

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!!IAA_SEQUENCE 1.0
ID RECA_SHISO STANDARD; PRT; 352 AA.
AC Q92FF6;
DT 15-DEC-1999 (Rel. 39, Created)
DT 15-DEC-1999 (Rel. 39, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
```

```

OS Shigella sonnei;
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Shigella.
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-KN1H104S;
RA PARK Y.C., SHIN H.J., KIM Y.C.;
RT "Cloning and nucleotide sequence of the recA gene from Shigella
sonnei KN1H104S.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF101227; AAC72856.1;
DR PROSITE; PS00321; RECA; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
FT INIT_MET 0 BY SIMILARITY.
FT NP_BIND 66 73 ATP (POTENTIAL).
SQ SEQUENCE 352 AA; 37799 MW; ADB29D96 CRC32;

RECA_SHISO Length: 352 April 26, 2000 08:21 Type: P Check: 8506

1 AIDENKOKAL AAALGQIEKQ FGKGSIMRLG EDRSMDVETI STGSLSLDIA
51 LGAGGLPMGR IVEIYGPESS GRTTLTLQVI AAAQLEGKTC AFIDAEHALD
101 PIYARKLGVD IDNLLCSQPD TGEQALEICD ALARSGAVDV INVDSVAALT
151 PKAEIEGEIG DSHMGLAARM MSQAMRKLAG NLKOSNILLI FNIQIRMKIG
201 VMFGNPETTT GGNALKFYAS VRLDIRRIGA VKEGENVVGS ETRVKVVKKN
251 IAAFPKQAEF QIILYGEINF YGELVDLVGK EKLIEKAGAW YSYKGEKIGQ
301 GKANATAWLK DNPETAKEIE KKVRELLLSN PNSTPDFSVD DSEGVAETNE
351 DF

AA_SEQUENCE 1.0
ID RECA_XENBV STANDARD; PRT; 358 AA.
AC P96185;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1999 (Rel. 39, Last sequence update)
DE RECA PROTEIN.
GN RECA.
OS Xenorhabdus bovienii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Xenorhabdus.
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-T228/1;
RA PINYON R.A., ORMSBY R., RALSTON H., THOMAS C.J.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.

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CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
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CC -----
DR EMBL; U87924; AAD12585.1;
DR HSSP; P03017; 2REB.
DR PROSITE; PS00321; RECA; 1.
DR PFAM; PF00154; RECA; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
FT NP_BIND 67 74 ATP (POTENTIAL).
SQ SEQUENCE 358 AA; 38487 MW; 3587853C CRC32;

RECA_XENBV Length: 358 April 26, 2000 08:21 Type: P Check: 6641

1 MANDENKOKA LAALGQIEK QFGKGSIMRL GENRSMDEVET ISTGSLSLDI
51 ALGAGGLPMG RIVEIYGPESS SGTTLTLQV IASAQREGKT CAFIDAEHAL
101 DPYIAKGLGV DIDNLLCSQP DTGEQALEIC DALSRSGAVD VIVVDSVAAL
151 TPKAIEIEGI GDHMGGLAAR MMSQAMRKLA GNLKNSNTLL IFINQIRMKI
201 GVWFGNPETT TGGNALKEYA SVRLDIRRTG SVKNGDEVVG SETRVKVVKN
251 KIAAPFKQAE FOILYGEIN TFGELVDLVG KHKWKEKAGA WYSYNGDKIG
301 QGKANATIYL KEHPEVSAEL DKKLRELLN NTGGFSSAYS DYVADYEDNG
351 EEVKNKEEF

AA_SEQUENCE 1.0
ID RECA_YERPE STANDARD; PRT; 356 AA.
AC P37858;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-W231;
RA KRYUKOV V.M., SUCHKOV I.Y., SAZYKIN I.S., MISHANKIN B.N.;
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC -----
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CC -----
DR EMBL; X75336; CAAS3084.1;
DR PIR; S37586; S37586.
DR HSSP; P03017; 2REB.
DR PROSITE; PS00321; RECA; 1.
DR PFAM; PF00154; RECA; 1.

```

KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
FT NP_BIND 67 74 ATP (BY SIMILARITY).
SQ SEQUENCE 356 AA; 37912 MW; 60B356BF CRC32;

RECA_YERPE Length: 356 April 26, 2000 08:21 Type: P Check: 8556 ..

1 MAIDENKOKA LAAALGQIEK QFGKGSIMRL GEDRSMDEVET ISTGSLSLDI
51 ALGAGGLPMG RIVEIYGPEK SKTTLTLQV IAAQREGKT CAFIDAEHAL
101 DPIYAKKLG V DIDNLLCSQP DTGEQALEIC DALTRSGAVD VIVDSVAAL
151 TPKEIEGEI GDHMGGLAAR MMSQAMKLA GNLNKNTLL IFINQIRMKI
201 GVMEGNPETT TGGNALKFYA SVRLDIRRG AVKGDGVVVG SETRVKVKVN
251 KIAAPFKQAE FQILYGBGIN INGELYDLGV KKLIEKAGA WYSYGDKIG
301 QGKANASNYL KENPANAAEL DKKLREMLN GNGEQPVAA ATAEFADGAD
351 ETNEEF

!!AA_SEQUENCE 1.0

ID Q9X5P5 PRELIMINARY; PRT; 358 AA.

AC Q9X5P5;

DT 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)

DE RECA PROTEIN.

OS RECA.

OS xenorhabdus nematophilus.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC xenorhabdus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-AM6;

RA HEW F.H., THOMAS C.J.;

RT "Analysis of the Xenorhabdus nematophilus AN6 recA gene sequence."

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases

CC FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE

CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF

CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT

CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS

CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC

CC CLEAVAGE.

EMBL: AF127333; AAD32599.1; ..

DR PROSITE; PS00321; RECA; 1.

KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.

SQ SEQUENCE 358 AA; 38586 MW; 51984C91 CRC32;

Q9X5P5 Length: 358 April 26, 2000 08:21 Type: P Check: 4576 ..

1 MANDENKOKA LAAALGQIEK QFGKGSIMRL GENRSMDEVET ISTGSLSLDI
51 ALGAGGLPMG RIVEIYGPEK SKTTLTLQV IAAQREGKT CAFIDAEHAL
101 DPVYAKKLG V DIDNLLCSQP DTGEQALEIC DALTRSGAVD VIVDSVAAL
151 TPKEIEGEI GDHMGGLAAR MMSQAMKLA GNLNKNTLL IFINQIRMKI
201 GVMEGNPETP PGGNALKFYA SVRLDIRRG SVKNGDEVVG SETRVKVKVN
251 KVAAPFKQAE FQILYGBGIN TLGELIDLSV KHKMVEKAGA WYSYNGDKIG
301 QGKANATIYL KERPETAEL NKKLRDLHLH NTGDFSSAAS DYVTDYEDNT
351 EVNNEEF

